

1	EARLIER	FILING DATE:	1997-08-22	
2	EARLIER	APPLICATION NUMBER:	60/056,562	
3	EARLIER	FILING DATE:	1997-08-22	
4	EARLIER	APPLICATION NUMBER:	60/056,872	
5	EARLIER	FILING DATE:	1997-08-22	
6	EARLIER	APPLICATION NUMBER:	60/056,982	
7	EARLIER	FILING DATE:	1997-08-22	
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9	EARLIER	FILING DATE:	1997-08-22	
10	EARLIER	APPLICATION NUMBER:	60/056,903	
11	EARLIER	FILING DATE:	1997-08-22	
12	EARLIER	APPLICATION NUMBER:	60/056,888	
13	EARLIER	FILING DATE:	1997-08-22	
14	EARLIER	APPLICATION NUMBER:	60/056,879	
15	EARLIER	FILING DATE:	1997-08-22	
16	EARLIER	APPLICATION NUMBER:	60/056,880	
17	EARLIER	FILING DATE:	1997-08-22	
18	EARLIER	APPLICATION NUMBER:	60/056,894	
19	EARLIER	FILING DATE:	1997-08-22	
20	EARLIER	APPLICATION NUMBER:	60/056,911	
21	EARLIER	FILING DATE:	1997-08-22	
22	EARLIER	APPLICATION NUMBER:	60/056,636	
23	EARLIER	FILING DATE:	1997-08-22	
24	EARLIER	APPLICATION NUMBER:	60/056,874	
25	EARLIER	FILING DATE:	1997-08-22	
26	EARLIER	APPLICATION NUMBER:	60/056,910	
27	EARLIER	FILING DATE:	1997-08-22	
28	EARLIER	APPLICATION NUMBER:	60/056,864	
29	EARLIER	FILING DATE:	1997-08-22	
30	EARLIER	APPLICATION NUMBER:	60/056,631	
31	EARLIER	FILING DATE:	1997-08-22	
32	EARLIER	APPLICATION NUMBER:	60/056,845	
33	EARLIER	FILING DATE:	1997-08-22	
34	EARLIER	APPLICATION NUMBER:	60/056,892	
35	EARLIER	FILING DATE:	1997-08-22	
36	EARLIER	APPLICATION NUMBER:	60/047,595	
37	EARLIER	FILING DATE:	1997-05-23	
38	EARLIER	APPLICATION NUMBER:	60/057,761	
39	EARLIER	FILING DATE:	05-Sep-1997	
40	EARLIER	APPLICATION NUMBER:	60/047,599	
41	EARLIER	FILING DATE:	1997-05-23	
42	EARLIER	APPLICATION NUMBER:	60/047,588	
43	EARLIER	FILING DATE:	1997-05-23	
44	EARLIER	APPLICATION NUMBER:	60/047,585	
45	EARLIER	FILING DATE:	1997-05-23	
46	EARLIER	APPLICATION NUMBER:	60/047,586	
47	EARLIER	FILING DATE:	1997-05-23	
48	EARLIER	APPLICATION NUMBER:	60/047,590	
49	EARLIER	FILING DATE:	1997-05-23	
50	EARLIER	APPLICATION NUMBER:	60/047,594	
51	EARLIER	FILING DATE:	1997-05-23	
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53	EARLIER	FILING DATE:	1997-05-23	
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55	EARLIER	FILING DATE:	1997-05-23	
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59	EARLIER	FILING DATE:	1997-04-11	
60	EARLIER	APPLICATION NUMBER:	60/043,576	
61	EARLIER	FILING DATE:	1997-04-11	
62	EARLIER	APPLICATION NUMBER:	60/047,501	
63	EARLIER	FILING DATE:	1997-05-23	
64	EARLIER	APPLICATION NUMBER:	60/043,670	
65	EARLIER	FILING DATE:	1997-04-11	
66	EARLIER	APPLICATION NUMBER:	60/056,632	
67	EARLIER	FILING DATE:	1997-08-22	
68	EARLIER	APPLICATION NUMBER:	60/056,664	
69	EARLIER	FILING DATE:	1997-08-22	
70	EARLIER	APPLICATION NUMBER:	60/056,876	
71	EARLIER	FILING DATE:	1997-08-22	
72	EARLIER	APPLICATION NUMBER:	60/056,881	
73	EARLIER	FILING DATE:	1997-08-22	

US-10-079-954-1 (1-297) x US-09-621-011-137 (1-233)

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Qy	181	CTCTCTCATCTCATTTGCTGAGGTTGCGAGCTGCTGTGTGCGCTTGGTGACACCAT	240
Db	84	LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaLeuValTyrThrThr	103
Qy	241	ATGGCTGAGACATTTCCGAGCTTCTGCTGGTAGTGCTGCCATCAAGAAG	288
Db	104	MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLvs	119

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; LABEL: EN1
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (233)
; OTHER INFORMATION: Xaa equals stop translation
US-09-621-011-137

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RESULT 3
US-08-808-148-1
; Sequence 1, Application US/08808148
; Patent No. 6020478
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer
; APPLICANT: Goli, Surya
; APPLICANT: Zhang, Hong Wolfe
; TITLE OF INVENTION: NOVEL HUMAN TUMOR-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,148
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0218 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSNOT26
; CLONE: 2187263
US-08-808-148-1

Alignment Scores:          9,61e-46          Length: 241
Pred. No.:                453.00           Matches: 93
Score:                     97.9%           Conservative: 1
Percent Similarity:        97.9%           Mismatches: 2
Best Local Similarity:     96.9%           Indels: 0
Query Match:               80.3%           Gaps: 0
DB:                         2

US-10-079-954-1 (1-297) x US-08-808-148-1 (1-241)

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33 SerleaspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerAlaMetGln 52
Qy 61 TTGTGCAACGTGGGCTACTTCTCATCGACCGCGGTGTGGTCTTTGCTTTGGTTTC 120
Db ::::|||||
53 PheValasnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72
Qy 121 CTGGGCTGCTATGCTTAAGACTGAGAGCAAGTGTGCCCTCGTGAGTCTTCTTCATC 180
Db ::::|||||
73 LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe 92
Qy 181 CTCCTCTCATCTTCATTCGTCGAGTTCGACGCTGCTGTGGTGGCTTGTACACCAT 240
Db ::::|||||
93 LeuLeuLeuIlePheIleAlaGluValAlaAlaValValAlaLeuValTyrThr 112
Qy 241 ATGGCTGAGCACTTCCCGACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 288
Db ::::|||||
113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

RESULT 4
US-09-020-956-114
; Sequence 114, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-020-956-114

Alignment Scores:          9,61e-46          Length: 241
Pred. No.:                453.00           Matches: 93
Score:                     97.9%           Conservative: 1
Percent Similarity:        97.9%           Mismatches: 2
Best Local Similarity:     96.9%           Indels: 0
Query Match:               80.3%           Gaps: 0
DB:                         2

US-10-079-954-1 (1-297) x US-09-020-956-114 (1-241)

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33 SerleaspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerAlaMetGln 52
Qy 61 TTGTGCAACGTGGGCTACTTCTCATCGACCGCGGTGTGGTCTTTGCTTTGGTTTC 120
Db ::::|||||
53 PheValasnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72
Qy 121 CTGGGCTGCTATGCTTAAGACTGAGAGCAAGTGTGCCCTCGTGAGTCTTCTTCATC 180
Db ::::|||||
73 LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe 92
Qy 181 CTCCTCTCATCTTCATTCGTCGAGTTCGACGCTGCTGTGGTGGCTTGTGTGTGTGTGTGTGTGTGTGT 240
Db ::::|||||
93 LeuLeuLeuIlePheIleAlaGluValAlaAlaValValAlaLeuValTyrThr 112
Qy 241 ATGGCTGAGCACTTCCCGACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 288
Db ::::|||||
113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

RESULT 5
US-09-030-607-114
; Sequence 114, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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Db 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

RESULT 8

US-09-232-149A-114

; Sequence 114, Application US/09232149A

; Patent No. 6465611

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.427C6

; CURRENT APPLICATION NUMBER: US/09/232.149A

; CURRENT FILING DATE: 1999-01-15

; NUMBER OF SEQ ID NOS: 338

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 114

; LENGTH: 241

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-232-149A-114

Alignment Scores:

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Score:	453.00	Matches:	93
Percent Similarity:	97.9%	Conservative:	1
Best Local Similarity:	96.9%	Mismatches:	2
Query Match:	80.3%	Indels:	0
DB:	2	Gaps:	0

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QY 61 TTGTCAACGTGGGCTACTTCTCATCGACCGCGGTGGTCTTGGCTCTTGGTTTC 120

Db 53 PheValAsnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72

QY 121 CTGGCTGCTATGCTGAAGACTGAGACGAGTGTGCCCTCGTGCACGCTTCTTCTCATC 180

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QY 181 CTCCTCTCATCTTCATGCTGAGTTGCGAGTGTGCTGTCGCTCGCCCTCGTGCACCATCA 240

Db 93 LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaLeuValTyrThrThr 112

QY 241 ATGGCTGAGCACTTCCCGACGTTGCTGCTAGTGCCTCGCCATCAAGAG 288

Db 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

RESULT 9

US-09-159-812-114

; Sequence 114, Application US/09159812A

; Patent No. 6613872

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF

; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.428C5

; CURRENT APPLICATION NUMBER: US/09/159,812A

; CURRENT FILING DATE: 1998-09-23

; NUMBER OF SEQ ID NOS: 306

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 114

; LENGTH: 241

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-159-812-114

Alignment Scores:

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Percent Similarity:	97.9%	Conservative:	1
Best Local Similarity:	96.9%	Mismatches:	2
Query Match:	80.3%	Indels:	0
DB:	2	Gaps:	0

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QY 61 TTGTCAACGTGGGCTACTTCTCATCGACCGCGGTGGTCTTGGCTCTTGGTTTC 120

Db 53 PheValAsnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72

QY 121 CTGGCTGCTATGCTGAAGACTGAGACGAGTGTGCCCTCGTGCACGCTTCTTCTCATC 180

Db 73 LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe 92

QY 181 CTCCTCTCATCTTCATGCTGAGTTGCGAGTGTGCTGTCGCTCGCCCTCGTGCACCATCA 240

Db 93 LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaLeuValTyrThrThr 112

QY 241 ATGGCTGAGCACTTCCCGACGTTGCTGCTAGTGCCTCGCCATCAAGAG 288

Db 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

RESULT 10

US-09-636-215-114

; Sequence 114, Application US/09636215

; Patent No. 6620922

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.42717C17

; CURRENT APPLICATION NUMBER: US/09/636,215

; CURRENT FILING DATE: 2000-08-10

; NUMBER OF SEQ ID NOS: 852

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 114

; LENGTH: 241

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-636-215-114

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DB:	2	Gaps:	0

Best Local Similarity: 96.9%
 Query Match: 80.3%
 DB: 2
 Mismatches: 2
 Indels: 0
 Gaps: 0

US-10-079-954-1 (1-297) x US-09-759-143-114 (1-241)

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Qy	61	TTTGTCAACGTGGGCTACTTCTCATCCAGCCGGTGTGGTCTTTGCTCTTGGTTTC	120
Db	53	PheValAsnValGlyTyrPheLeuIleAlaAlaGlyValValValPheAlaLeuGlyPhe	72
Qy	121	CTGGGCTGCTATGGTGTAAAGACTGAGAGCAAGTGTGCCCTCGTGAGCTTCTTCTTCATC	180
Db	73	LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePheIle	92
Qy	181	CTCCTCTCATCTTCATTGCTGAGGTTGCAGCTGTGTGGTGGCTTGGTGTACACCATTA	240
Db	93	LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaLeuValTyrThrThr	112
Qy	241	ATGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCTGCATCAAGAAG	288
Db	113	MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys	128

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:40:14 ; Search time 3.60161 Seconds
(without alignments)
1394.518 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

Searched: 263416 seqs, 96216763 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: pir2.*
3: pir3.*
4: pir4.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	69	13.7	424	2	F71087 hypothetical prote
4	69	13.7	1700	2	S08167 Balbani ring 3 pr
5	67.5	13.4	1515	2	S51824 myosin heavy chain
6	66.5	13.2	770	2	S60676 cellobiose oxidase
7	66.5	13.2	1057	1	ORTR atrial natriuretic
8	66.5	13.2	1057	2	I55319 guanylyl cyclase A
9	66.5	13.2	1057	2	I57963 natriuretic peptid
10	66	13.1	372	1	H0ECSN hydrogenase (EC 1.
11	66	13.1	372	2	D85632 hydrogenase-1 smal
12	66	13.1	372	2	H90769 hydrogenase-1 smal
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21	65	12.9	430	2	T14536
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27	64	12.7	350	2	AG1407
28	64	12.7	350	2	AG1783
29	64	12.7	627	4	A40201
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31	64	12.7	811	2	S08579
32	63.5	12.6	104	2	AC2099
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37	63.5	12.6	640	2	S49932
38	63.5	12.6	768	2	D97626
39	63.5	12.6	772	2	D96504
40	63.5	12.6	900	2	T07717
41	63.5	12.6	990	2	T03784
42	63.5	12.6	1057	1	OYMSAR
43	63.5	12.6	1902	2	C97702
44	63.5	12.6	2318	2	S45306
45	63.5	12.6	4660	2	T42737

ALIGNMENTS

RESULT 1

JC7110
brain-specific membrane anchor protein - human
C:Species: Homo sapiens (man)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: JC7110
R:Eison, G.C.A.; de Coignac, A.B.; Aubry, J.P.; Delneste, Y.; Magistrelli, G.; Holzwarth
Biochem. Biophys. Res. Commun. 264, 55-62, 1999
A:Title: BSMAP, a novel protein expressed specifically in the brain whose gene is local
A:Reference number: JC7110; MUID:99458621; PMID:10527841
A:Accession: JC7110
A:Molecule type: mRNA
A:Residues: 1-342 <EL>
A:Cross-references: UNIPROT:Q9UK28; UNIPARC:UPI0000034024; GB:AF186264; NID:96003653; PI
C:Genetics:
A:Gene: bsmap
A:Map position: 19p12
C:Superfamily: human brain-specific membrane anchor protein
C:Keywords: brain; glycoprotein; membrane bound; transmembrane protein

Alignment Scores:			
Pred. No.:	6.99	Length:	342
Score:	72.50	Matches:	24
Percent Similarity:	45.0%	Conservative:	12
Best Local Similarity:	30.0%	Mismatches:	29
Query Match:	14.4%	Indels:	15
DB:	2	Gaps:	4

US-10-079-954-2 (1-261) x JC7110 (1-342)

Qy	22	GACATAGAGTGGTGTGTCATGCTTGAGAGAGAAACACTTTCGAGTCCAGAACCCA	81
Db	69	AspArgAlaValLeulleSerAlaCysGluarg	84
Qy	82	AGGAGGTGCAATGG	114
Db	85	SerIleCysArgPheValAlaArgSerSerLysProAsnAlaThrGlnThrGluCysGlu	104

zinc finger protei
hepatocyte growth
50S ribosomal prot
N-acetylglucosamin
DNA (cytosine-5)-
S-locus-specific g
S-locus-specific g
plasmin (EC 3.4.21
myelin transcripti
ubiquitin thiolest
hypothetical prote
hypothetical prote
sorbitol dehydroge
sorbitol dehydroge
artifect-warnin g
malate dehydrogena
hypothetical prote
hypothetical prote
DHNA phythltransfe
hypothetical prote
hypothetical prote
alpha-1-microglu
cbid protein - Syn
MET30 protein - ye
hypothetical prote
protein F9C16.25
probable ABC-type
probable receptor
atrial natriuretic
cell surface anti
notch 3 protein -
gp330 protein prec

Qy 115 ATAGCGCGCGTGAATATTTCCAGCTTTTTCATGGTTCCCAACAGGTGCTCCGCTGCT 174
Db 105 AlaAlaCysValGluAlaTyrrVallys---GluAlaGluGlnGlnAlaCysSerHisGly 123
Qy 175 TGT---GCAGCGATGAGAGACCAAGCGAGGAGGAGCGGTTCTCTCCAGAGAGGCC 231
Db 124 CysTrpSerGlnProAlaGluProGluProGluGlnLysArgLysValLeuGluAlaPro 143

RESULT 2
B70503
probable pyrG protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: B70503
R:Colo, S.T.; Davies, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Biles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: B70503
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-586 <COL>
A:Cross-references: UNIPROT:p96351; UNIPARC:UPI0000132D70; GB:Z98268; GB:AL123456; NID:9
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: pyrG
C:Superfamily: CTP synthase

Alignment Scores:
Pred. No.: 10.3 Length: 586
Score: 71.00 Matches: 20
Percent Similarity: 42.3% Conservative: 10
Best Local Similarity: 28.2% Mismatches: 31
Query Match: 14.1% Indels: 10
DB: 2 Gaps: 1

US-10-079-954-2 (1-261) x B70503 (1-586)

Qy 66 CGAGTCCAGAACCAACGAG-----GTGCMAATG 95
Db 294 ArgValHisGluProHisGluThrValArgLeuAlaLeuValGlyLysValGluLeu 313
Qy 96 GACAGAGCCATCTCGGTTATAGCGCGGTGAAATATTTCCACGTTTTTCATGGTTCG 155
Db 314 SerAspAlaTyrrLeuSerValAlaGluAlaLeuArgAlaGlyGlyPheLysHisArgAla 333
Qy 156 CAACAGGTGCTCGGTTGTGCGATGGAGAGACCAAGCCAGCGAGAGAGCGGTT 215
Db 334 LysValGluIleCysTrpValAlaSerAspGlyCysGluThrThrSerGlyAlaAlaAla 353
Qy 216 TCTCTGGAGAGCCGCTTCCTTTTACCT 248
Db 354 AlaLeuGlyAspValHisGlyValLeuIlePro 364

RESULT 3
F71087
hypothetical protein PH0963 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: F71087
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: F71087
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-424 <KAW>
A:Cross-references: UNIPROT:058701; UNIPARC:UPI0000139E88; GB:AP000004; NID:93236131; PJ

A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0963

Alignment Scores:
Pred. No.: 17.5 Length: 424
Score: 69.00 Matches: 27
Percent Similarity: 41.1% Conservative: 12
Best Local Similarity: 23.4% Mismatches: 21
Query Match: 13.7% Indels: 35
DB: 2 Gaps: 3

US-10-079-954-2 (1-261) x F71087 (1-424).

Qy 72 CCAGAACCAAGAGGTGCAATAGCAGACGACCATCTCGGTTAT----- 116
Db 22 ProValLysLysGluLeuGluLeuThrLysPheLeuLeuLysTyrrLysAspLysProVal 41
Qy 117 -----AGCGCGCGTGAATAAT 131
Db 42 LeuPheLysAspValGluGlyTrpGluValAlaGlyAsnLeuTrpSerArgGluArg 61
Qy 132 ATTCCACGTTTTTCATGGTTCCCAACAGGTGCTCCGCTGGTTGTGCA-----GGCAT 185
Db 62 IleAlaLysPheLeuAsnThrAspAsnLysGlyLeuLeuGluLeu-LeuTyrrGluAlaMe 81
Qy 186 GGAGAGACCAACGCA-----GAGGAGAA 209
Db 81 tGluLysProLysProPheSerValValGluLysAlaGluPheLeuLysAsnArgGluLy 101
Qy 210 GCGGTTTCTCTGGAGAGCCCATGCCCTTCTTTTACTCTCAAG 252
Db 101 sValAsnLeuLeuGluLeuProIleProLysTyrrTyrrProLys 115

RESULT 4
S08167
Balbiani ring 3 protein - midge (Chironomus tentans)
C:Species: Chironomus tentans
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Aug-2004
C:Accession: S08167
R:Paulsson, G.; Lendahl, U.; Galli, J.; Ericsson, C.; Wieslander, L.
J. Mol. Biol. 211, 331-349, 1990
A:Title: The balbiani ring 3 gene in Chironomus tentans has a diverged repetitive struct
A:Reference number: S08167; MUID:90172404; PMID:1689777
A:Accession: S08167
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-1700 <PAU>
A:Cross-references: UNIPROT:Q03376; UNIPARC:UPI0000126788; GB:X52263; NID:97057; PIDN:CA
C:Genetics:
A:Gene: BR3
A:Map position: 4

Alignment Scores:
Pred. No.: 17.4 Length: 1700
Score: 69.00 Matches: 20
Percent Similarity: 41.2% Conservative: 15
Best Local Similarity: 23.5% Mismatches: 36
Query Match: 13.7% Indels: 14
DB: 2 Gaps: 4

US-10-079-954-2 (1-261) x S08167 (1-1700)

Qy 22 GACAATAGAGTGGTGTGTCATGCTTGTGAGAGAGAAACACTTTCGAGTGCAGAACCCA 81
Db 946 AspAsnLeuCysGlnCysGluCysLysAsnLysGlnGluMetAlaAsnCysLysSerPro 965
Qy 82 AGGAGGTGCAATAGCAGAGCCCATCTCGGTTATAGCGCGCGTGA--- 129
Db 966 ArgThrTrpAsnTyrrAspThrCysLysValCysValCysLysAsnAlaAspAspSerAspAsp 985
Qy 130 ---ATAATTCCACGTTTTTTTTCATGGTTTCGCAACAGGTGCTCCGCTGGTTGT---GCAGCG 183

A: Residues: 1-363, H: 367-391, F: 393-1077 <DMM>
A: Cross-references: UNIPARC:UPI0000170968; GB:U7535; NID:G204269; PIDN:AAA4120
C:Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain
C:Keywords: ATP; carbon-oxygen lyase; cGMP biosynthesis; glycoprotein; hormone
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-1057/Product: atrial natriuretic peptide receptor #status predicted <MAT>
F:29-469/Domain: extracellular #status predicted <EXT>
F:109-449/Domain: natriuretic peptide-binding domain homology <NPB>
F:470-490/Domain: transmembrane #status predicted <TM>
F:491-1057/Domain: intracellular #status predicted <INT>
F:522-804/Domain: protein kinase homology <KIN>
F:824-1051/Domain: guanylate cyclase catalytic domain homology <GCC>
F:41,208,334,375,382,423/Binding site: carbohydrate (Asn) #status predicted <AS>

Alignment Scores:	33.6	Length:	1057
Pred. No.:	66.50	Matches:	27
Score:			

A;Gene: hyaA	
C;Superfamily: hydrogenase (NiFe) small chain	
Alignment Scores:	
Pred. No.:	38.5
Score:	66.00
Length:	372
Percent Similarity:	40.3%
Matches:	21
Best Local Similarity:	29.2%
Conservative:	8
Query Match:	13.1%
Mismatches:	19
Indels:	24
Gaps:	4
DB:	2
US-10-079-954-2 (1-261) x D85632 (1-372)	

```

43 AlaIrpAlaLeuGluuGluuLysPProAGIleProValValIrpIle-----
QY      175 AACCAAGCGGAGCACTCTTTCGGAACCATGAAAAAACGTGGAAATATTTTCACGG-----
Db      175 |||||
59 GlyLeuGluCysThrCysCys-----ThrGluSerPheIleArgSer
QY      175 |||||
Db      175 |||||
121 ---CGGTATPAACGCAGTATGGCTCTGTCTCATTTGACACCTCTCTGGGTTCCTGGCAC
QY      121 |||||
Db      121 |||||
74 HisProLeuAlaLysAspValIleLeuSerLeu-----
QY      74 |||||
Db      74 |||||
64 AAGTGTTCCTCTCTCAACAGCATGACACCACTC 29
QY      64 |||||
Db      64 |||||
85 -----IleSerLeuAspGlyTrpAspGlyThrLeu 93
QY      85 -----
Db      85 -----

```

RESULT 12
H90769
hydrogenase-1 small subunit [imported] - Escherichia coli (strain O157
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-
R:Accession: H90769
R:Author: T. Makino, K. Ohnishi, M. Kurokawa, K. Ishii, K. Yokota,
R:Havashi, T. Makino, K. Ohnishi, M. Kurokawa, K. Ishii, K. Yokota,

Gasegawa, N.; Tasunaga, I.; Kunara, S.; Sniba, I.; Maffori, M.; Shinada, T. *Journal of Bacteriology* 1999, 191, 1035-1041.
 A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: H90769
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-372 <HAY>
 A:Cross-references: UNIPROT:Q8XC39; UNIPARC:UPI00000D050E; GB:BA000007
 A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Gene: ECs1128
 C:Superfamily: hydrogenase (NiFe) small chain

Alignment Scores:					
Pred. No.:	38.5	Length:	372		
Score:	66.00	Matches:	21		
Percent Similarity:	40.3%	Conservative:	8		
Best Local Similarity:	29.2%	Mismatches:	19		
Query Match:	13.1%	Indels:	24		
DB:	2	Gaps:	4		
 US-10-079-954-2 (1-261) x H90769 (1-372)					
Qy	235	GCATGGGCTCTCCAGGAGAAACCGTCTCTCCTGGGTGGGTCTCTCCATCGCT			
Dd	43	AAtRPaLaueGuAenYsProARgIlePrOvalrPile-----			
Qy	175	AACCAGCGGACACTGTTTCGAACCACTGAAAAAAACGTGGAAATAATTTTCA CGG-			

121	QY	---CCGCTATAACGCAAGTAGGCTCTGTCTCATTTGCACCTCTTGGGTTCTGGCAC
74	Db	HisProLeuAlaIysAspValIleLeuSerLeu-----
64	QY	AAGTGTGTTTCTCTCTCACAGCATGACACCACTC 29

```
Db 85 -----IleSerLeuAspTyrAspAspThrLeu 93
:::||||| :::||||| |||||
US-10-079-954-2 (1-261) x T46637 (1-1187)

RESULT 13
T30189
myelin transcription factor 1 homolog - mouse
N:Alternate names: zinc finger protein Myt1l
C:Species: Mus musculus (house mouse)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30189
R:Kim, J.G.; Armstrong, R.C.; Robinsky, A.; Agoston, D.V.; Wiese, C.; Nagle, J.; Hudson, J. Neurosci. Res. 50: 272-290, 1997
A:Title: Myelin transcription factor 1 (Myt1) of the oligodendrocyte lineage, along with
.
A:Reference number: Z20766; MUID:98038874; PMID:9373037
A:Accession: T30189
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1182 <KIM>
A:Cross-references: UNIPROT:O08996; UNIPARC:UPI00000E71E5; EMBL:AF004295; NID:G2624928;

Alignment Scores:
Pred. No.: 38.3 Length: 1182
Score: 66.00 Matches: 21
Percent Similarity: 44.8% Conservative: 5
Best Local Similarity: 36.2% Mismatches: 20
Query Match: 13.1% Indels: 12
DB: 2 Gaps: 3

US-10-079-954-2 (1-261) x T30189 (1-1182)
Qy 86 GGTGCAATGACAGAGCCATCTAGCGTTATAGCGCGGTGAAATATTTCCAGTGTTC 145
||| :::||||| |||||
Db 954 GlyCysAspGlyGlnGlyHisIleThr-----GlyLysTyrAlaSerHisArg 969

Qy 146 TCATGTTTCGCAACAGGTGCTCCGCTGTGTGCAGCGATGGAGAGACCCCAAGCCAGG 205
||| :::||||| |||||
Db 970 Ser-----AlaSerGlyCysProLeuAlaAlaLysArgGlnLysAspGlyTyrLeuAsn 987

Qy 206 AGAAGCGGTTTCTCTCGAAGAGC-----CCATGCCCTTCT 241
||| ||||| ||||| |||||
Db 988 GlySerGlnPheSerTrpLysSerValLysThrGluGlyMetSerCysProThr 1005

RESULT 14
T46637
transcription factor 1, neural - rat
N:Alternate names: neural zinc finger factor-1
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46637
R:Jiang, Y.; Yu, V.C.; Buchholz, F.; O'Connell, S.; Rhodes, S.J.; Candeloro, C.; Xia, Y. J. Biol. Chem. 271, 10723-10730, 1996
A:Title: A novel family of Cys-Cys, His-Cys zinc finger transcription factors expressed
A:Reference number: A58210; MUID:96210003; PMID:8631881
A:Accession: T46637
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1187 <JIA>
A:Cross-references: UNIPROT:P70475; UNIPARC:UPI00000E86A7; EMBL:U48809; NID:G1511631; PI
A:Gene: NZF-1
C:Function:
A:Description: binds specifically to a cis-regulatory element of the beta-retinoic acid
nervous system and in the pituitary gland
C:Keywords: DNA binding; transcription factor

Alignment Scores:
Pred. No.: 38.3 Length: 1187
Score: 66.00 Matches: 21
Percent Similarity: 44.8% Conservative: 5
Best Local Similarity: 36.2% Mismatches: 20
Query Match: 13.1% Indels: 12
DB: 2 Gaps: 3
```

```
US-10-079-954-2 (1-261) x T46637 (1-1187)
Qy 86 GGTGCAATGACAGAGCCATCTAGCGTTATAGCGCGGTGAAATATTTCCAGTGTTC 145
||| :::||||| |||||
Db 957 GlyCysAspGlyGlnGlyHisIleThr-----GlyLysTyrAlaSerHisArg 972

Qy 146 TCATGTTTCGCAACAGGTGCTCCGCTGTGTGCAGCGATGGAGAGACCCCAAGCCAGG 205
||| :::||||| |||||
Db 973 Ser-----AlaSerGlyCysProLeuAlaAlaLysArgGlnLysAspGlyTyrLeuAsn 990

Qy 206 AGAAGCGGTTTCTCTCGAAGAGC-----CCATGCCCTTCT 241
||| ||||| ||||| |||||
Db 991 GlySerGlnPheSerTrpLysSerValLysThrGluGlyMetSerCysProThr 1008

RESULT 15
T46608
zinc finger protein Png-1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46608
R>Weiner, J.; Chun, J. J. Comp. Neurol. 381, 130-142, 1997
A:Title: Png-1, a nervous system-specific zinc finger gene, identifies regions containing
A:Reference number: Z23102; MUID:97276971; PMID:9130664
A:Accession: T46608
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1188 <WEI>
A:Cross-references: UNIPROT:P97500; UNIPARC:UPI000002912B; EMBL:U86339; NID:G1835754; PI
A:Experimental source: strain BALB/c
C:Genetics:
A:Gene: Png-1

Alignment Scores:
Pred. No.: 38.3 Length: 1188
Score: 66.00 Matches: 21
Percent Similarity: 44.8% Conservative: 5
Best Local Similarity: 36.2% Mismatches: 20
Query Match: 13.1% Indels: 12
DB: 2 Gaps: 3

US-10-079-954-2 (1-261) x T46608 (1-1188)
Qy 86 GGTGCAATGACAGAGCCATCTAGCGTTATAGCGCGGTGAAATATTTCCAGTGTTC 145
||| :::||||| |||||
Db 960 GlyCysAspGlyGlnGlyHisIleThr-----GlyLysTyrAlaSerHisArg 975

Qy 146 TCATGTTTCGCAACAGGTGCTCCGCTGTGTGCAGCGATGGAGAGACCCCAAGCCAGG 205
||| :::||||| |||||
Db 976 Ser-----AlaSerGlyCysProLeuAlaAlaLysArgGlnLysAspGlyTyrLeuAsn 993

Qy 206 AGAAGCGGTTTCTCTCGAAGAGC-----CCATGCCCTTCT 241
||| ||||| ||||| |||||
Db 994 GlySerGlnPheSerTrpLysSerValLysThrGluGlyMetSerCysProThr 1011

Search completed: March 23, 2006, 12:47:18
Job time : 23.0081 secs
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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:33:09 ; Search time 16.5581 Seconds
(without alignments)
2224.208 Million cell updates/sec

Title: US-10-079-954-2
Perfect score: 502
Sequence: 1 agccaggaacgacgagg.....tttacctaaagtgtgtaa 261

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/abs8/ABSSWEB/spool/US10079954/runat_23032006_102929_1793/app_query.fasta_1
-DE=uniprot -QFWT=fastcan -SUFFIX=rup -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORES=500 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HRAPIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs802p
-USER=US10079954 @CGN 1.1.580 @runat_23032006_102929_1793 -NCPU=6 -ICPU=3
-NO_WMAP -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	482	96.0	179	2	Q9BVD7 HUMAN	Q9bvd7 homo sapien
2	478	95.2	224	2	O15227 HUMAN	O15227 homo sapien
3	205	40.8	154	2	Q9CWP4 MOUSE	Q9cwp4 mus musculus
4	110.5	22.0	176	2	Q9QU55 MOUSE	Q9qu55 mus musculus
5	97.5	19.4	158	1	GML HUMAN	G99445 homo sapien
6	96.5	19.2	176	2	Q9DAP4 MOUSE	Q9dap4 mus musculus
7	81	16.1	310	2	Q7S5T7 NEUCRA	Q7s5t7 neurospora
8	80	15.9	583	2	Q740ES MYCBA	Q740es mycobacteri
9	78.5	15.6	201	2	Q45211 TETNG	Q45211 tetraodon n
10	77.5	15.4	472	2	Q978V2 THEVO	Q978v2 thermoplasm
11	77.5	15.4	493	2	Q6KZ09 PICTO	Q6kz09 picophilus
12	76	15.1	251	2	Q4J5Z9 AZOVI	Q4j5z9 azotobacter
13	76	15.1	1475	2	Q7N7V2 PHOLL	Q7n7v2 photorhabdu
14	73	14.5	317	2	Q6D9G3 ERWCT	Q6d9g3 erwinia car
15	73	14.5	326	2	Q7X844 ORISA	Q7x844 oryza sativ
16	73	14.5	345	2	Q4SC28 TETNG	Q4sc28 tetraodon n

17	72.5	14.4	342	1	BSMAP HUMAN	Q9uk28 homo sapien
18	72	14.3	554	2	O57473 XENLA	O57473 xenopus lae
c 19	71.5	14.2	350	2	O5A300 CANAL	O5a300 candida alb
c 20	71.5	14.2	589	2	O8NDX2 HUMAN	O8ndx2 homo sapien
21	71.5	14.2	1474	2	Q8GFP9 PHOLU	Q8gfp9 photorhabdu
22	71	14.1	449	2	Q6YTJ0 ORISA	Q6ytj0 oryza sativ
23	71	14.1	586	1	PYRG MYCTU	P0a5u3 mycobacteri
24	71	14.1	586	1	PYRG MYCTU	P0a5u2 mycobacteri
25	71	14.1	1145	2	O6C7Y9 YARLI	O6c7y9 yarrowia li
26	70.5	14.0	97	2	O86SR0 HUMAN	O86sr0 homo sapien
27	70.5	14.0	131	2	O8NSJ9 HUMAN	O8nsj9 homo sapien
28	70.5	14.0	336	2	Q873P9 MUCMU	Q873p9 mucor muced
c 29	70.5	14.0	485	2	Q9HLC1 THEAC	Q9hlc1 thermoplasm
c 30	70	13.9	120	2	Q4T8C6 TETNG	Q4t8c6 tetraodon n
c 31	70	13.9	369	2	Q4LZG8 BURK	Q4lzg8 burkholderi
c 32	70	13.9	503	2	Q9LSC6 ARATH	Q9lsc6 arabidopsis
c 33	70	13.9	534	2	Q4WG10 ASPFU	Q4wg10 aspergillus
34	70	13.9	1704	2	Q94446 DUFT	Q94446 chironomus
c 35	69.5	13.8	294	2	Q53VX1 THETH	Q53vx1 thermus the
c 36	69.5	13.8	411	2	Q50Q35 ENTHI	Q50q35 entamoeba h
c 37	69	13.7	309	2	Q7F1K9 ORISA	Q7f1k9 oryza sativ
c 38	69	13.7	375	1	MBHS CITFR	Q46045 citrobacter
39	69	13.7	424	1	Y963 PYRHO	O58701 pyrococcus
c 40	69	13.7	500	2	Q891J6 BRAJA	Q891j6 bradyrhizob
c 41	69	13.7	763	1	RINI MOUSE	Q921q7 mus musculu
c 42	69	13.7	1003	2	Q6AUV7 ORISA	Q6auv7 oryza sativ
43	69	13.7	1700	1	BAR3 CHITE	Q03376 chironomus
44	68.5	13.6	139	1	LY6H MOUSE	Q9wuc3 mus musculu
45	68.5	13.6	139	2	Q544M1 MOUSE	Q544m1 mus musculu

ALIGNMENTS

RESULT 1
Q9BVD7_HUMAN
ID Q9BVD7_HUMAN PRELIMINARY; PRT; 179 AA.
AC Q9BVD7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE LY6K protein (Fragment).
GN Name=LY6K;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cervix;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences".
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Cervix;
 RA Director MGC Project;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC001291; AA001291.2; -; mRNA.
 DR Ensembl; ENSG00000160886; Homo sapiens.
 FT NON_TER 1
 SQ SEQUENCE 179 AA; 20060 MW; A80B96DFEA691E8D CRC64;

Alignment Scores:

Pred. No.: 4.68e-46 Length: 179
 Score: 482.00 Matches: 83
 Percent Similarity: 96.6% Conservative: 1
 Best Local Similarity: 95.4% Mismatches: 3
 Query Match: 96.0% Indels: 0
 DB: 2 Gaps: 0

US-10-079-954-2 (1-261) x Q9BVD7_HUMAN (1-179)

QY 1 ACCGAGCGACGAGCGGTGACAAATAGAGTGTGGTGTCTGTCATGCTGTGTGAGAGAGAAAC 60
 Db 45 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 64
 QY 61 ACTTTTCGAGTGCAGAACCCAGAGAGGTGCAATCGACAGAGCCATCTGCGTTATAGCG 120
 Db 65 ThrPheGluCysGlnAsnProhArgCysLysTrpThrGluProTyCysValIleAla 84
 QY 121 GCCGTGAAATATTTCCACGTTTTTCATGTTTCGCAACAGAGTCTCCGCTGGTGTGCA 180
 Db 85 AlaValIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 104
 QY 181 GCGATGGAGAGCCCAAGCCAGAGAGCGGTCTCTCTGGAAGAGCCATGCCCTTC 240
 Db 105 AlaMetGluArgProLysProGluGluLysArgPheLeuGluGluProMetProphe 124
 QY 241 TTTTACCTCAAGTGTGTAAA 261
 Db 125 PheTyLeuLysCysCysLys 131

RESULT 2

O15227_HUMAN
 ID O15227_HUMAN PRELIMINARY; PRT; 224 AA.
 AC O15227
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CO16 protein (Fragment).
 GN Name=LY6K; Synonyms=CO16;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Machl A.W., Plantzter S.A., Ruckels M., Kubbies M.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ001348; CA04692.1; -; mRNA.
 DR Ensembl; ENSG00000160886; Homo sapiens.
 DR HGNC; HGNC:24225; LY6K.
 FT NON_TER 224
 SQ SEQUENCE 224 AA; 25175 MW; C14BB9F680E0D59D CRC64;

Alignment Scores:

Pred. No.: 1.39e-45 Length: 224
 Score: 478.00 Matches: 82
 Percent Similarity: 95.4% Conservative: 1
 Best Local Similarity: 94.3% Mismatches: 4
 Query Match: 95.2% Indels: 0
 DB: 2 Gaps: 0

US-10-079-954-2 (1-261) x O15227_HUMAN (1-224)

QY 1 ACCGAGCGACGAGCGGTGACAAATAGAGTGTGGTGTCTGTCATGCTGTGTGAGAGAGAAAC 60

Db 89 SerGlnArgThrAspGluGlyAspAsnArgAlaTrpCysHisValCysGluArgGluAsn 108
 QY 61 ACTTTTCGAGTGCAGAACCCAGAGAGGTGCAATCGACAGAGCCATCTGCGTTATAGCG 120
 Db 109 ThrPheGluCysGlnAsnProArgCysLysTrpThrGluProTyCysValIleAla 128
 QY 121 GCCGTGAAATATTTCCACGTTTTTCATGTTTCGCAACAGAGTCTCCGCTGGTGTGCA 180
 Db 129 AlaValIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 148
 QY 181 GCGATGGAGAGCCCAAGCCAGAGAGCGGTCTCTCTGGAAGAGCCATGCCCTTC 240
 Db 149 AlaMetGluArgProLysProGluGluLysArgPheLeuGluGluProMetProphe 168
 QY 241 TTTTACCTCAAGTGTGTAAA 261
 Db 169 PheTyLeuLysCysCysLys 175

RESULT 3
 Q9CWP4_MOUSE
 ID Q9CWP4_MOUSE PRELIMINARY; PRT; 154 AA.
 AC Q9CWP4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Mus musculus ES cells cDNA, RIKEN full-length enriched library,
 DE clone:2410015A16 product:hypothetical CD59 antigen containing protein,
 DE full insert sequence (2410015A16Rik protein).
 GN Name=Ly6k;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RA Carninci P., Hayashizaki Y.;
 RL MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Iehi Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RL "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RA MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikola I., Osato N., Saito R., Suzuki H., Yamanaka I., Yamanaka H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grinstead S., Guscinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maita L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., King B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Vervardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito R., Saito C., Sakai K., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Beak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Harte S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Sanches A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Straube R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
REMBL; AK010485; BAB26976.1; -: mRNA.
DR EMBL; BC049723; AAH49723.1; -: mRNA.
DR Ensembl; ENSMUSG0000044678; Mus musculus.
DR MGI; MGI:1923736; Ly6k.
DR InterPro; IPR001526; LY6 UPAR.
DR InterPro; IPR008197; WAP.
DR PRINTS; PR00003; 4DISULPHORE.
DR SMART; SM00134; LU; 1.
RW Hypothetical protein.
SQ SEQUENCE 154 AA; 17134 MW; F756FBB2B3B400C6 CRC64;
Alignment Scores:
Pred. No.: 2,54e-14 Length: 154
Score: 205.00 Matches: 33
Percent Similarity: 57.6% Conservative: 16
Best Local Similarity: 38.8% Mismatches: 30
Query Match: 40.8% Indels: 6
DB: 2 Gaps: 1
US-10-079-954-2 (1-261) x Q9CWP4_MOUSE (1-154)
Qy 25 AATAGAGTGTGGTCTATGCTTGTGAGAGAGAAACTTTCGAGTCCGACCAAGG 84
Db 19 AShAlaLeuThrCysHisValCysGluAlaAsnSerTyrAlaCysSerAsnProSer 38
Qy 85 AGTGCAGAAATGGACAGAGCCATCTCGTTATAGCGCCGCGTAAATATTTCCACGTTT 144
Db 39 GlnCysProGlyGluLysLysPheCysLeuLeuAlaValThrArgIlePheGluArgPhe 58
Qy 145 TTCATGTTGCGCAACAGGTCTCGCTGTGTGTGCAGCG-----ATG 186
Db 59 PheTyrValSerLysGlnCysThrArgArgCysProThrProValValSerProProSer 78
Qy 187 GAGAGACCCCAAGCCAGGAGAGAGCGGTTTCTCTCGAAGAGCCCATGCGCTTTTAC 246
Db 79 ThrAsnProProSerGluProLysGluPheLeuIleGluLysProMetProPheLeuPhe 98
Qy 247 CTCAGTGTGTGATAA 261
Db 99 TyrLysCysGln 103
RESULT 4
Q9CUL5_MOUSE
ID Q9CUL5_MOUSE PRELIMINARY; PRT; 176 AA.
AC Q9CUL5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE HemT-3 protein.
GN Name=HemT;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

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OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=9250249; PubMed=10231568; DOI=10.1016/S0378-1119(99)00099-2;
RA Xue H., O'Neill D., Morrow J., Bank A.;
RL Gene 231:49-58(1999).
RT "A novel mouse gene, HemT, encoding an hematopoietic cell-specific
transcript.";
RN NUCLEOTIDE SEQUENCE.
RA Xue H., O'Neill D., Wang X., Wolgemuth D., Bank A.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ242831; CAB57316.1; -; mRNA.
DR EMBL; AJ242830; CAB57315.1; -; Genomic_DNA.
DR InterPro; IPR001526; LY6_UPAR.
DR SMART; SM00134; LU; 1.
SQ SEQUENCE 176 AA; 20170 MW; 85584EE92EDE275E CRC64;

Alignment Scores:
Pred. No.: 0.00176 Length: 176
Score: 110.50 Matches: 24
Percent Similarity: 45.5% Conservative: 16
Best Local Similarity: 27.3% Mismatches: 39
Query Match: 22.0% Indels: 9
Db: 2 Gaps: 3

US-10-079-954-2 (1-261) x Q9QUL5_MOUSE (1-176)
QY 22 GACATAGAGTG-----TGG-----TGCTGCTGTGTGAGAGAGAA 57
Db 36 AspaenAlaIleGluProArgTrpThrProGlnMetArgCysHisSerCysGlnGluHis 55
QY 58 AACACTTTCGATGCCAGAACCCAGAGGTGCAATGACAGAGCCCATCTACGCGTTATA 117
Db 56 AnThrPheTyrcysProHisIleHisTyrcysAspMetAspIleArgCysLeuThr 75
QY 118 GCGGCGGTGAAATATTTCCAGCTTTTTCATGTTCCACAGGTGCTCCGCTGGTGT 177
Db 76 ValAlaIleArgValAsnIleArgLeuLeuTyValLeuLysAspCysThrLysAspCys 95
QY 178 GCAGCGATGAGAGAGACCCCAAG---CCAGAGAGAGAGCGGTTCTCTCGAAGAGCCCATG 234
Db 96 ThrPheIleTyrcysGluHisValProGlnLeuProArgValLeuLysAspValLys 115
QY 235 CCCTCTTTTACCTCAAGTGTGT 258
Db 116 AnPheTyrcysPheValMetCysCys 123

RESULT 5
GML_HUMAN
ID GML_HUMAN STANDARD; PRT; 158 AA.
AC Q99445; O00686; O00731;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Glycosyl-phosphatidylinositol-anchored molecule-like protein
DE precursor.
GN Name=GML; Synonyms=LY6DL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=97088635; PubMed=8914543;
RA Furuhashi T., Tokino T., Urano T., Nakamura Y.;
RT "Isolation of a novel GPI-anchored gene specifically regulated by p53;
correlation between its expression and anti-cancer drug sensitivity.";
RN Oncogene 13:1965-1970(1996).
RP NUCLEOTIDE SEQUENCE.
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RX MEDLINE=97312709; PubMed=9169150; DOI=10.1006/geno.1997.4680;
RA Kimura Y., Furuhashi T., Urano T., Hirata K., Nakamura Y., Tokino T.;
RT "Genomic structure and chromosomal localization of GML (GPI-anchored
molecule-like protein), a gene induced by p53.";
RL Genomics 41:477-480(1997).
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: May play a role in the apoptotic pathway or cell-cycle
regulation induced by p53 after DNA damage.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
(Potential).
CC -1- INDUCTION: By p53.
CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
DR EMBL; D84290; BAA12300.1; -; mRNA.
DR EMBL; AB000381; BAA19961.1; -; Genomic_DNA.
DR EMBL; BC074930; AAH74930.1; -; mRNA.
DR Ensembl; ENSG00000104499; Homo sapiens.
DR HGNC; HGNC:4375; GML.
DR MIM; 602370; -.
DR GO; GO:0019898; C:extrinsic to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0006915; P:apoptosis; TAS.
DR GO; GO:0006977; P:DNA damage response, signal transduction by...; TAS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR GO; GO:0000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR001526; LY6_UPAR.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; LY6_UPAR; 1.
KW GPI-anchor; Lipoprotein; Membrane; Polymorphism; Signal.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 158 Glycosyl-phosphatidylinositol-anchored
molecule-like protein.
FT DOMAIN 29 134 UPAR/Ly6.
FT DISULFID 31 55 By similarity.
FT DISULFID 34 42 By similarity.
FT DISULFID 48 73 By similarity.
FT DISULFID 77 104 By similarity.
FT DISULFID 105 110 By similarity.
FT VARIANT 54 54 R -> C (in dbSNP:3764795).
FT /FTID=VAR_020174.
SQ SEQUENCE 158 AA; 17730 MW; 21D7F23D33DBB3B2 CRC64;

Alignment Scores:
Pred. No.: 0.0534 Length: 158
Score: 97.50 Matches: 23
```


Percent Similarity: 46.2% Conservatives: 13
 Best Local Similarity: 29.5% Mismatches: 35
 Query Match: 19.4% Indels: 7
 DB: 1 Gaps: 2

US-10-079-954-2 (1-261) x GML_HUMAN (1-158)

QY 37 TGTCATGCTTGTGAGAGAAACACTTTTCGAGTGCAGACCCCAAGAGGTGCAGATGG 96
 Db CysHisAspCysAlaValIleAsnAspPheAsnCysProAsnIleArgValCysProTyr 50
 QY 97 ACAGAGCCATACGCTGTTATAGCGCGCTGAAATATTTCCAGCTTTTTCATGGTTCGC 156
 Db HisIleArgA-gCysMetThrIleSerIleArgIleAsnSerArgGluLeuLeuValTyr 70
 QY 157 AACAGGTCTCGCTGGTGTGT- - - - -GCAGCGATGAGAGACCCCAAGCCAGAG 204
 Db LysAsnCysThrAsnAsnCysThrPheValTyrAlaIleGluInProProGluAlaPro 90
 QY 205 GAGAGCGGTTCTCTCGAGAGAGCCGATGCTTTTACCTCAAGTGTGT 258
 Db GlyLysIlePhe- - - - -LysThrAsnSerPheTyrTrpValCysCys 105

RESULT 6

Q9DAP4_MOUSE
 ID Q9DAP4_MOUSE PRELIMINARY; PRT; 176 AA.
 AC Q9DAP4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
 library, clone:1700003p22 product:hematopoietic cell transcript 1,
 full insert sequence.
 GN Name=Hem1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OX Muridae; Murinae; Mus.
 NCBI TaxID=10090;
 [1]
 RP NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 [2]

RP NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischer M., Gaasterland T., Gissi C., King B., Kochiwa H.,
 Kuhl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,
 Blake J., Boirelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [3]
 RP NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6J; TISSUE=Testis;

RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [4]
 RN NUCLEOTIDE SEQUENCE
 RP STRAIN=C57BL/6J; TISSUE=Testis;
 RC MEDLINE=20499374; PubMed=1042159; DOI=10.1101/gr.145100;
 RX Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RA "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RN NUCLEOTIDE SEQUENCE
 RP STRAIN=C57BL/6J; TISSUE=Testis;
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RX Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RA "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RN NUCLEOTIDE SEQUENCE
 RP STRAIN=C57BL/6J; TISSUE=Testis;
 RC Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
 Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K., Sakai K.,
 Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 Muramatsu M., Hayashizaki Y.;
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK005659; BAB24171.1; -; mRNA.
 DR MGI; MGI:1341831; Hemt1.
 DR InterPro; IPR001526; LY6_UPAR.
 DR SMART; SM00134; LU; 1.
 SQ SEQUENCE 176 AA; 19890 MW; 8D595E54A7A5C3A6 CRC64;
 Alignment Scores:
 Pred. No.: 0.0707 Length: 176
 Score: 96.50 Matches: 23
 Percent Similarity: 40.9% Conservatives: 13
 Best Local Similarity: 26.1% Mismatches: 43
 Query Match: 19.2% Indels: 9
 DB: 2 Gaps: 3
 US-10-079-954-2 (1-261) x Q9DAP4_MOUSE (1-176)
 QY 22 GACAAATAGAGT- - - - -TGCATGCTTGTGAGAGAGAA 57
 Db CysHisAspCysAlaValIleAsnAspPheAsnCysProAsnIleArgValCysProTyr 55
 QY 58 AACACTTTCGAGTGCAGACCCCAAGAGGTGCAGACCCCAAGAGGTGCAGATGGTATA 117
 Db HisIleArgA-gCysMetThrIleSerIleArgIleAsnSerArgGluLeuLeuValTyr 75
 QY 118 GCGCGCGTGAATAATATTTCCAGCTTTTTCATGCTTCGCAACAGGTGCTCGGTGTGT 177
 Db ValSerPheArgValIleAsnIleArgLeuLeuTyrValLeuLysAspCysThrLysAspCys 95
 QY 178 GCAGCGATGGAGAGACCCCAAG- - -CCAGAGGAGAGCGGTTTCTCTGGAGAGCCCATG 234

OC Thermoplasmataceae; Thermoplasma.
 ON NCBI_TaxID=50339;
 OX [1]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SSSI / DSM 4299 / JCM 9571;
 RX MEDLINE=20570466; PubMed=11121031; DOI=10.1073/pnas.97.26.14257;
 RA Kawashima T., Amano N., Kolihe K., Makino S.-I., Higuchi S.,
 RA Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
 RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
 RT "Archaeal adaptation to higher temperatures revealed by genomic
 sequence of Thermoplasma volcanium";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
 DR EMBL; BA000011; BAB60455.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 472 AA; 52179 MW; 951318097D49B169 CRC64;

Alignment Scores:
 Pred. No.: 12.4 Length: 472
 Score: 77.50 Matches: 24
 Percent Similarity: 45.1% Conservative: 8
 Best Local Similarity: 33.8% Mismatches: 32
 Query Match: 15.4% Indels: 7
 DB: 2 Gaps: 2

US-10-079-954-2 (1-261) x Q97HV2_THEVO (1-472)

QY 201 TGGCTTGGGTCTCTCCATCGCTGCACACACGGGAGCACCTTGTGGCAACCATGAAAAA 142
 |||||
 DB 223 TptlleGlyGlyProLeuThrGlyThrGlyThrSerGly-----ValSerSerllelleGly 240
 |||||
 QY 141 ACGTGGAAATATTTTCACGGCGGTATACGCGATGATGGCTCTGTCCATTTGACACTCTCT 82
 |||||
 DB 241 ThrTpGlyLysPhePheGlyLeuTrpSerAlaValTrpPheThrValThrProPro 260
 |||||
 QY 81 TGGGTTCTGGCACTCGCAAGTGTTCCTCTCTCACAGCATG-----ACA 37
 |||||
 DB 261 SerValSerValIleGlyLysThrAlaThrValThrSerMetAsnGlnPheIleValThr 280
 |||||
 QY 36 CCACACTCTATTGTCAACCCTCGCTCGGTTCGCTG 4
 |||||
 DB 281 ProThrSerAlaAsnAsnThrValGluTyrLeu 291
 |||||

RESULT 11
 Q6KZ09 PICTO
 ID Q6KZ09 PICTO PRELIMINARY; PRT; 493 AA.
 AC Q6KZ09
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Membrane associated protein.
 GN OrderedLocustNames=PTO1458;
 OS Picrophilus torridus.
 OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
 OC Picrophilaceae; Picrophilus.
 ON NCBI_TaxID=82076;
 OX [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=DSM 9790 / ATCC 700027;
 RX PubMed=15184674; DOI=10.1073/pnas.0401356101;
 RA Fuetteler O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,
 RA Schepers B., Dock C., Antranikian G., Liebl W.;
 RT "Genome sequence of Picrophilus torridus and its implications for life
 around pH 0";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
 DR EMBL; AE017261; AAR44043.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 493 AA; 55374 MW; 6985D7468592F363 CRC64;

Alignment Scores:
 Pred. No.: 12.5 Length: 493
 Score: 77.50 Matches: 23
 Percent Similarity: 46.6% Conservative: 11
 Best Local Similarity: 31.5% Mismatches: 32

Search completed: March 23, 2006, 12:45:56
Job time : 87.7903 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:29:14 ; Search time 19.271 Seconds
(without alignments)

1190.162 Million cell updates/sec

Title: US-10-079-954-2

Perfect score: 502

Sequence: 1 agccagcgaacgacgaggg.....tttacctcaagtgtgttaa 261

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/abs/ABSSWEB.spool/US10079954/runat_23032006_102927_1781/app_query.fasta_1
-DB=A.GeneSeq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -DOOPCL=0 -DOOEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=Blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HRAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02p
-USER=US10079954 @CGN 1.1 476 @runat_23032006_102927_1781 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -BSPBLOCK=100 -JONGLOG -DEVI TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A.GeneSeq 21.*
1: GeneSeq1980s.*
2: GeneSeq1990s.*
3: GeneSeq2000s.*
4: GeneSeq2001s.*
5: GeneSeq2002s.*
6: GeneSeq2003as.*
7: GeneSeq2003bs.*
8: GeneSeq2004s.*
9: GeneSeq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	482	96.0	162	5 ABP42766	Human ova
2	482	96.0	165	5 ABG61944	Prostate
3	482	96.0	165	6 ABUS56446	Lung canc
4	482	96.0	165	7 ADN39436	Cancer/an
5	482	96.0	166	8 ADU06395	Novel bro
6	482	96.0	223	2 AAU81754	Human Fan
7	482	96.0	223	6 ABR48226	Human bla
8	482	96.0	223	6 ABUS56671	Lung canc
9	482	96.0	223	7 ADN39022	Cancer/an

10	482	96.0	248	7 ADF60487	Human con
11	482	96.0	248	8 ADS12252	Human the
12	375	74.7	171	7 ADF59395	Human pol
13	371.5	74.0	162	8 ADS11037	Human the
14	205	40.8	154	5 ADI17070	Murine NO
15	97.5	19.4	158	2 AAU36523	GPI ancho
16	81	16.1	240	8 ADN21057	Bacterial
17	80	15.9	583	6 ABU33887	Protein e
18	78.5	15.6	342	7 ADA45175	Human pol
19	77	15.3	106	4 AAU62645	Propionib
20	77	15.3	106	6 ABMS9164	Propionib
21	76	15.1	136	6 ABR41162	Human DiT
22	76	15.1	1476	6 ABM70222	Photothab
23	75	14.9	159	7 ABO79796	Pseudomon
24	75	14.9	636	6 ABUL7389	Protein e
25	73	14.5	136	7 ABO71446	Pseudomon
26	72.5	14.4	286	7 ADG14985	Human SEC
27	72.5	14.4	309	8 ADJ66975	Human sec
28	72.5	14.4	342	2 AAY16785	Human sec
29	72.5	14.4	342	3 AAB00163	Brain spe
30	72.5	14.4	353	4 AAM25782	Human pro
31	72.5	14.4	3011	2 AAR95021	Hepatitis
32	71.5	14.2	588	6 AAE32079	Human TRI
33	71.5	14.2	589	5 AAU93329	Human tra
34	71.5	14.2	589	6 AAU30994	Human tra
35	71.5	14.2	589	7 ADD01392	Human TCH
36	71.5	14.2	589	7 ADG88329	Human tra
37	71.5	14.2	589	8 ADR10021	Human pro
38	71.5	14.2	1474	8 ADP18622	Photothab
39	71.5	14.2	1474	8 ADR21525	Photothab
40	71	14.1	543	6 ABU34884	Protein e
41	71	14.1	586	6 ABU36674	Protein e
42	70.5	14.0	97	3 AAY87278	Human sig
43	70.5	14.0	97	3 AAB18912	A novel p
44	70.5	14.0	97	4 AAU29257	Human PRO
45	70.5	14.0	97	6 ABUS8633	Human PRO

ALIGNMENTS

RESULT 1

ABP42766
ID ABP42766 standard; protein; 162 AA.

XX AC ABP42766;

XX AC ABP42766;
XX DT 22-AUG-2002 (first entry)

XX DE Human ovarian antigen HOVK66, SEQ ID NO:3898.

XX KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
XX KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
XX KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
XX KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
XX KW inflammatory condition; immune disorder; blood disorder;
XX KW cardiovascular disorder; respiratory disorder; neurological disorder;
XX KW gastrointestinal disorder; urinary system disorder; drug screening;
XX KW gene therapy; chromosome mapping; forensic analysis;
XX KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
XX KW antiinflammatory; gynaecological; reproductive.

XX OS Homo sapiens.

XX OS WO200200677-A1.

XX PD 03-JAN-2002.

XX PF 07-JUN-2001; 2001WO-US018569.

XX PR 07-JUN-2000; 2000US-0209467P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX

QY 1 AGCCAGCGAACGGACGAGGTGCACAATAGAGTGTGGTGTCATGCTTTGTGAGAGAGAAAAC 60
Db |||||
QY 31 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAen 50
Db |||||
QY 61 ACTTTTCAGTGCACGAACCCACGAGGAGTGC AAAATGGACGAGCCATACTCGGTTATAGCG 120
Db |||||
QY 51 ThrPheGluCysGlnAsnProArgCysLysIrpThrGluProTyrCysValIleAla 70
Db |||||
QY 121 GCCGTGAAAAATATTTCCACGTTTTTTTCATGCTTCGCCAACAGGTGCTCCGCTGGTTGTGCA 180
Db |||||
QY 71 AlaValGlyIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 90
Db |||||
QY 181 GCGATGGAGAGACCCACGACGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTC 240
Db |||||
QY 91 AlaMetGluArgProLysProGluGluLysArgPheLeuLeuGluGluProMetProPhe 110
Db |||||
QY 241 TTTTACCTCAAGTGTGTAA 261
Db |||||
QY 111 PheTyrLeuLysCysCysLys 117
Db |||||

RESULT 3

ID ABU56446

ID ABU56446 standard; protein; 165 AA.

XX ABU56446;

XX AC

XX XX

DT 02-APR-2003 (first entry)

DE Lung cancer-associated polypeptide #39.

XX

XX Lung cancer-associated polypeptide; cytostatic; emphysema;
 XX antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX

OS Unidentified.

XX

PN WO200286443-A2.

XX

PD 31-OCT-2002.

XX

PF 18-APR-2002; 2002WO-US012476.

XX

PR 18-APR-2001; 2001US-0284770P.

XX

PR 10-MAY-2001; 2001US-0290492P.

PR 09-NOV-2001; 2001US-0339245P.

PR 13-NOV-2001; 2001US-0350666P.

PR 29-NOV-2001; 2001US-0334370P.

PR 12-APR-2002; 2002US-0372246P.

XX

PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX

PI Aziz N, Murray R;

XX

DR WPI; 2003-093161/08.

DR N-PSDB; ABX76167.

XX

XX Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer.

XX

PS Claim 27; Page 220; 453pp; English.

XX

XX The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridises
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung cancer-
 CC associated polynucleotides and polypeptides are used for identifying a
 CC compound that modulates a lung cancer-associated polypeptide, for

PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-035250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-039775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilton KE, Zlotnik A;
XX WPI; 2003-468649/44.
DR N-PSDB; ADN39435.
XX Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX Claim 12; SEQ ID NO A36; 1385pp; English.
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX SQ Sequence 165 AA;

Alignment Scores:
Pred. No.: 1.7e-47 Length: 165
Score: 482.00 Matches: 83
Percent Similarity: 96.6% Conservative: 1
Best Local Similarity: 95.4% Mismatches: 3
Query Match: 96.0% Indels: 0
DB: 7 Gaps: 0

US-10-079-954-2 (1-261) x ADN39436 (1-165)

QY 1 AGCCAGCCGACGAGGGTGACATAGAGTGGTGTCTGCTGTGAGAGGAAAC 60
DB 31 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 50
QY 61 ACTTTCGAGTGCAGAACCCAGAGAGGTGCAATGAGAGCCATAGTGGTGTATAGCG 120
DB 51 ThrPheGluCysGlnAsnProArgCysIleTrpThrGluProTrpCysValIleAla 70
QY 121 GCCGTGAAATATTTCCAGTGTTCATGTTTCAGTTCGCAACAGAGTCTCCGCTGGTGTGCA 180
DB 71 AlaValIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 90

QY 181 GCGATGGAGAGACCCCAAGCCAGAGGAGAGCGGTTTCTCTCGAAGAGCCATGCCCTTC 240
DB 91 AlawetGluArgProLysProGluGluLysArgPheLeuLeuGluGluProMetProPhe 110
QY 241 TTTTACCTCAAGTGTGTAA 261
DB 111 PheTyrLeuLysCysCysLys 117
RESULT 5
ADU06395
ID ADU06395 standard; protein; 166 AA.
XX AC ADU06395;
XX 27-JAN-2005 (first entry)
XX Novel bronchial cancer-associated human protein SeqID619.
XX bronchial cancer; cytostatic; tumour-associated protein;
KW cancer detection; metastasis; tumour; human.
XX Homo sapiens.
XX DE10316701-A1.
XX 04-NOV-2004.
XX 09-APR-2003; 2003DE-01016701.
XX 09-APR-2003; 2003DE-01016701.
XX (HINZ/) HINZMANN B.
XX (HERM/) HERMANN K.
XX (CAST/) HEIDEN CASTANOS-VELEZ E.
XX Mennerich D, Bruemendorf T, Heiden E, Hermann K, Kinnemann H;
PI Li X, Roepcke S, Staub E, Hinzmann B, Rosenthal A, Pilarsky C;
XX WPI; 2004-786403/78.
DR N-PSDB; ADU05908.

New nucleic acid, and derived proteins, useful for diagnosis of bronchial cancer and in screening for therapeutic and diagnostic agents.
Claim 2; SEQ ID NO 619; 1381pp; German.

This invention relates to a novel isolated nucleic acid associated with bronchial cancer comprising 489 defined sequences given in the specification. The invention may be useful for the production of compounds with a cytostatic activity through the inhibition of expression or activity of tumour-associated proteins. The novel DNA sequences and the proteins/peptides encoded by them are used for detecting bronchial cancer or determining the risk of developing it and to screen for specific binding partners of the DNA or protein sequences, where the binding partners are potentially useful as agents for treating or diagnosing bronchial cancer. The DNA or protein sequences can also be used for prognosis, detection of metastases and for secondary treatment (of tumours that have been stabilised or are no longer detectable). Detecting abnormal expression of the DNA sequences provides early diagnosis of bronchial cancers. The present sequence is that of a protein encoded by a novel bronchial cancer-associated human gene sequence of the invention.

SQ Sequence 166 AA;

Alignment Scores:
Pred. No.: 1.71e-47 Length: 166
Score: 482.00 Matches: 83
Percent Similarity: 96.6% Conservative: 1
Best Local Similarity: 95.4% Mismatches: 3
Query Match: 96.0% Indels: 0
DB: 8 Gaps: 0

US-10-079-954-2 (1-261) x ADU06395 (1-166)

QY 1 AGCCAGCGAAGCGAGGGTGACATAGAGTGTGGTGTGTCATGTCGAGAGAGAAAC 60
 Db 31 SerGlnargThrAspGluGlyAspAsnargValTrpCysHisValCysGluargGluAsn 50
 QY 61 ACTTTCGAGTGCACAGAACCCAGAGGGTGCAATGAGAGAGCCATCTGCGTTATAGCG 120
 Db 51 ThrPheGluCysGlnAsnProargCysLysTrpThrGluProTrpCysValIleAla 70
 QY 121 GCCGTGAAATATTTCCAGGTTTTTTCATGTTCCCAACAGAGTGTCTCGCTGGTTGTGCA 180
 Db 71 AlaValLysIlePheProargPheMetValAlaLysGlnCysSerAlaGlyCysAla 90
 QY 181 GCGATGGAGAGACCCAGAGAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTC 240
 Db 91 AlaMetGluargProLysPheGluGlyLysArgPheLeuLeuGluLuprometProphe 110
 QY 241 TTTTACCTCAAGTGTGTAA 261
 Db 111 PheTyrLeuLysCysCysLys 117

RESULT 6

AAW81754
 ID AAW81754 standard; protein; 223 AA.
 AC AAW81754;
 XX

DT 27-JAN-1999 (first entry)

XX Human Fanconi anaemia-associated gene II protein.

XX Fanconi anaemia gene II; immunogen; diagnosis; detection; disease;
 KW cell cycle; disorder; cell activation; DNA repair; cytopaenia;
 KW gene therapy; tumorigenesis.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Misc-difference 79
 FT Misc-difference /label= unknown
 FT Misc-difference 87
 FT Misc-difference /label= unknown

XX WO9845428-A1.
 XX 15-OCT-1998.
 XX 06-APR-1998; 98WO-EP001994.
 XX 07-APR-1997; 97EP-00105688.
 XX (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX Kubbies M, Machl A, Planitzer S;
 DR WPI; 1998-568348/48.
 DR N-PSDB; AAV64572.

XX New human Fanconi anaemia associated gene-II - useful for diagnosis,
 FT treatment and prevention of diseases associated with abnormal cell
 FT cycling or activation, DNA repair, cytopaenia, tumorigenesis etc.
 XX
 PS Claim 9; Page 20; 35pp; German.

XX This sequence represents a protein which is associated with Fanconi
 CC anaemia. This protein can be used as an immunogen for preparation of
 CC antibodies. This sequence can be used for diagnosis of, or detecting
 CC predisposition to, diseases that involve disorders of the cell cycle,
 CC cell activation, cell cycle progression, DNA repair, cytopaenia,
 CC tumorigenesis and/or tumour progression, also for treatment and
 CC prevention of these diseases, particularly by gene therapy

SQ Sequence 223 AA;

Alignment Scores:
 Pred. No.: 1.84e-47 Length: 223
 Score: 482.00 Matches: 83
 Percent Similarity: 96.6% Conservative: 1
 Best Local Similarity: 95.4% Mismatches: 3
 Query Match: 96.0% Indels: 0
 DB: 2 Gaps: 0

US-10-079-954-2 (1-261) x AAW81754 (1-223)

QY 1 AGCCAGCGAAGCGAGGGTGACATAGAGTGTGGTGTGTCATGTCGAGAGAGAAAC 60
 Db 89 SerGlnargThrAspGluGlyAspAsnargValTrpCysHisValCysGluargGluAsn 108
 QY 61 ACTTTCGAGTGCACAGAACCCAGAGGGTGCAATGAGAGAGCCATCTGCGTTATAGCG 120
 Db 109 ThrPheGluCysGlnAsnProargCysLysTrpThrGluProTrpCysValIleAla 128
 QY 121 GCCGTGAAATATTTCCAGGTTTTTTCATGTTCCCAACAGAGTGTCTCGCTGGTTGTGCA 180
 Db 129 AlaValLysIlePheProargPheMetValAlaLysGlnCysSerAlaGlyCysAla 148
 QY 181 GCGATGGAGAGACCCAGAGAGAGAGCGGTTTCTCTGGAAGAGCCCATGCCCTTC 240
 Db 149 AlaMetGluargProLysPheGluGlyLysArgPheLeuLeuGluLuprometProphe 168
 QY 241 TTTTACCTCAAGTGTGTAA 261
 Db 169 PheTyrLeuLysCysCysLys 175

RESULT 7

ABR48226
 ID ABR48226 standard; protein; 223 AA.
 XX AC ABR48226;
 XX

DT 12-JUN-2003 (first entry)

XX Human bladder cancer associated protein sequence SEQ ID NO:173.

XX Human; bladder cancer; cytostatic; gene therapy; vaccine.

OS Homo sapiens.

FN WO2003003906-A2.

XX 16-JAN-2003.

XX 03-JUL-2002; 2002WO-US021338.

XX 03-JUL-2001; 2001US-0302814P.

FR 03-AUG-2001; 2001US-0310099P.

PR 08-NOV-2001; 2001US-0343705P.

PR 13-NOV-2001; 2001US-0350666P.

XX 12-APR-2002; 2002US-0372246P.

XX (E0SB-) EOS BIOTECHNOLOGY INC.

XX Mack DH, Aziz N;

PI WPI; 2003-201532/19.

XX N-PSDB; ACC51042.

DR DR

XX

PT Detecting a bladder cancer-associated transcript in a cell from a
 PT patient, comprises contacting a biological sample from the patient with a
 PT bladder cancer-associated polynucleotide or antibody.

PS Claim 10; Page 289; 307pp; English.

XX The present invention describes a method for detecting a bladder cancer-
 CC associated transcript in a cell from a patient. The method comprises

CC contacting a biological sample from the patient with a polynucleotide
CC that selectively hybridises to a sequence that is 80 % identical to a
CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
CC encode the human bladder cancer-associated proteins given in ABR48146 to
CC ABR48242). Bladder cancer-associated sequences from the present invention
CC have cytostatic activities, and can be used in antisense gene therapy and
CC in vaccine production. The method can be used for detecting a bladder
CC cancer-associated transcript in a cell from a patient. The method is
CC useful in diagnosing or treating bladder cancer and in screening for
CC compounds that modulate bladder cancer, such as hormones or antibodies.
CC The nucleic acid molecules from the present invention may be used in
CC various screening and diagnostic methods, and for gene therapy, vaccine
CC and/or antisense/inhibition applications
XX
SQ Sequence 223 AA;

Alignment Scores:
Pred. No.: 1.84e-47 Length: 223
Score: 482.00 Matches: 83
Percent Similarity: 96.6% Conservative: 1
Best Local Similarity: 95.4% Mismatches: 3
Query Match: 96.0% Indels: 0
DB: 6 Gaps: 0

US-10-079-954-2 (1-261) x ABR48226 (1-223)

QY 1 AGCCAGCGACGACGAGGGTGACATAGAGTGTGTCTCATGTGTGAGAGAGAAAC 60
DB 89 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 108
QY 61 ACTTTCGAGTCCGACACCCAGGAGGTCGAAATGACAGAGCCATCTCGTGTATAGCG 120
DB 109 ThrPheGluCysGlnAsnProArgArgCysIstPrThrGluProTrpCysValIleAla 128
QY 121 GCGGTGAAATATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTGCA 180
DB 129 AlaValIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 148
QY 181 GCGATGGAGAGACCCAGCCAGAGAGAGAGCGGTTTCTCTGGAGAGCCCATGCCCTTC 240
DB 149 AlaMetGluArgProLysProGluGlyArgPheLeuLeuGluGluProMetProphe 168
QY 241 TTTTACCTCAAGTGTGTAAA 261
DB 169 PheTyrLeuLysCysCysLys 175

RESULT 8

ABU56671
ID ABU56671 standard; protein; 223 AA.

XX AC ABU56671;

XX DT 02-APR-2003 (first entry)

XX DE Lung cancer-associated polypeptide #264.

XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;
XX antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX OS Unidentified.

XX PN WO200286443-A2.

XX PD 31-OCT-2002.

XX PF 18-APR-2002; 2002WO-US012476.

XX PR 18-APR-2001; 2001US-0284770P.

XX PR 10-MAY-2001; 2001US-0290492P.

XX PR 09-NOV-2001; 2001US-0339245P.

PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
XX 12-APR-2002; 2002US-0372246P.
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Aziz N, Murray R;

XX WPI; 2003-093161/08.

DR N-PSDB; ABX76400.

XX Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.

XX Claim 27; Page 392; 453pp; English.

XX The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABU56408-ABU56745 represent lung cancer-associated polypeptides of the
CC invention

SQ Sequence 223 AA;

Alignment Scores:
Pred. No.: 1.84e-47 Length: 223
Score: 482.00 Matches: 83
Percent Similarity: 96.6% Conservative: 1
Best Local Similarity: 95.4% Mismatches: 3
Query Match: 96.0% Indels: 0
DB: 6 Gaps: 0

US-10-079-954-2 (1-261) x ABU56671 (1-223)

QY 1 AGCCAGCGACGACGAGGGTGACATAGAGTGTGTCTCATGTGTGAGAGAGAAAC 60
DB 89 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 108
QY 61 ACTTTCGAGTCCGACACCCAGGAGGTCGAAATGACAGAGCCATCTCGTGTATAGCG 120
DB 109 ThrPheGluCysGlnAsnProArgArgCysIstPrThrGluProTrpCysValIleAla 128
QY 121 GCGGTGAAATATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTGCA 180
DB 129 AlaValIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 148
QY 181 GCGATGGAGAGACCCAGCCAGAGAGAGAGCGGTTTCTCTGGAGAGCCCATGCCCTTC 240
DB 149 AlaMetGluArgProLysProGluGlyArgPheLeuLeuGluGluProMetProphe 168
QY 241 TTTTACCTCAAGTGTGTAAA 261
DB 169 PheTyrLeuLysCysCysLys 175

RESULT 9

ADN39022

ID ADN39022 standard; protein; 223 AA.

CC a host cell genetically engineered to comprise (I) which is operatively
 CC associated with a regulatory sequence that modulates expression of (I) in
 CC the host cell; (4) a polypeptide (II) encoded by (I); (5) a composition
 CC comprising the polypeptide of (4) and a carrier; (6) an antibody directed
 CC against the polypeptide of (4); (7) detecting (I) or the polypeptide of
 CC (4) in a sample; (8) identifying a compound that binds to the polypeptide
 CC of (4); (9) producing the polypeptide of (4); and (10) a collection of
 CC polynucleotides comprising at least one of the polynucleotide sequences
 CC (I). The polynucleotides (I) can be used as hybridisation probes,
 CC oligomers or primers, for chromosome or gene mapping, for the recombinant
 CC production of proteins, and for generating antisense DNA or RNA. The
 CC present sequence represents a human contig polypeptide sequence, which is
 CC used in an example from the present invention.

XX SQ Sequence 248 AA;

Alignment Scores: 1.89e-47 Length: 248
 Pred. No.: 482.00 Matches: 83
 Score: 96.6% Conservative: 1
 Percent Similarity: 95.4% Mismatches: 3
 Best Local Similarity: 96.0% Indels: 0
 Query Match: 7 Gaps: 0
 DB:

US-10-079-954-2 (1-261) x ADF60487 (1-248)

Qy 1 AGCCAGCGAAGCGAGCGGTGACATAGAGTGTGGTGTCTGCTGTGAGAGAGAAAC 60
 Db 89 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 108
 Qy 61 ACTTTCGAGTCCAGACCCAGAGCGGTGCAATAGAGTGTGGTGTCTGCTGTGAGAGAGAAAC 120
 Db 109 ThrPheGluCysGlnAsnProArgArgCysLysTrpThrGluProTyrCysValIleAla 128
 Qy 121 GCCGTGAAATATTTCCACGTTTTTCATGCTGCGCAACAGGTGCTCGCTGGTGTGCA 180
 Db 129 AlaValIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 148
 Qy 181 GCGATGGAGAGACCCAGAGCGGTGCAATAGAGTGTGGTGTCTGCTGTGAGAGAGAAAC 240
 Db 149 AlaMetGluArgProLysProGluGlyArgPheLeuLeuGluGluProMetProPhe 168
 Qy 241 TTTTACCTCAAGTGTGTAAA 261
 Db 169 PheTyrLeuLysCysCysLys 175

RESULT 11

ADSI12252

ID ADSI12252 standard; protein; 248 AA.

XX AC ADSI12252;

XX DT 16-DEC-2004 (first entry)

XX DE Human therapeutic contig protein - SEQ ID 2489.

XX KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;
 XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
 KW aplastic anaemia; cancer; wound healing; gene therapy.

OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 1..248

FT /label= Unknown, OTHER

FT /note= "OTHER = In-frame stop codon"

XX PN WO2004080148-A2.

XX PD 23-SEP-2004.

XX PF 30-SEP-2003; 2003WO-US030720.

XX

PR 02-OCT-2002; 2002US-0416186P.

XX PA (NUVE-) NUVELO INC.

XX PI Tang YT, Asundi V, Ren P, Zhang J, Wehrman T, Wang Z, Ma Y;

XX PT Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;

XX DR WPI; 2004-658857/65.

XX DR N-PSDB; ADSI1654.

XX PT New polynucleotide, useful in preparing a composition for diagnosing or
 XX treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
 XX aplastic anemia or cancer for promoting wound healing.

XX Example 2; SEQ ID NO 2489; 718pp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded
 CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
 CC neuroprotective, antianaemic, cytostatic and vulnery activities and may
 CC be useful in preparing a composition for diagnosing or treating
 CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
 CC disorders, such as aplastic anaemia or cancer, as well as for promoting
 CC wound healing. The molecules may also be utilised during gene therapy
 CC procedures. The current sequence is that of a human therapeutic contig
 CC protein of the invention.

XX SQ Sequence 248 AA;

Alignment Scores: 1.89e-47 Length: 248
 Pred. No.: 482.00 Matches: 83
 Score: 96.6% Conservative: 1
 Percent Similarity: 95.4% Mismatches: 3
 Best Local Similarity: 96.0% Indels: 0
 Query Match: 8 Gaps: 0
 DB:

US-10-079-954-2 (1-261) x ADSI12252 (1-248)

Qy 1 AGCCAGCGAAGCGAGCGGTGACATAGAGTGTGGTGTCTGCTGTGAGAGAGAAAC 60

Db 89 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 108

Qy 61 ACTTTCGAGTCCAGACCCAGAGCGGTGCAATAGAGTGTGGTGTCTGCTGTGAGAGAGAAAC 120

Db 109 ThrPheGluCysGlnAsnProArgArgCysLysTrpThrGluProTyrCysValIleAla 128

Qy 121 GCCGTGAAATATTTCCACGTTTTTCATGCTGCGCAACAGGTGCTCGCTGGTGTGCA 180

Db 129 AlaValIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 148

Qy 181 GCGATGGAGAGACCCAGAGCGGTGCAATAGAGTGTGGTGTCTGCTGTGAGAGAGAAAC 240

Db 149 AlaMetGluArgProLysProGluGlyArgPheLeuLeuGluGluProMetProPhe 168

Qy 241 TTTTACCTCAAGTGTGTAAA 261

Db 169 PheTyrLeuLysCysCysLys 175

RESULT 12

ADFS9395

ID ADFS9395 standard; protein; 171 AA.

XX AC ADFS9395;

XX DT 12-FEB-2004 (first entry)

XX DE Human polypeptide sequence SEQ ID NO:1803.

XX KW biological activity; genetic engineering; hybridisation probe; oligomer;
 KW primer; chromosome mapping; gene mapping; recombinant protein production;
 XX human.

XX OS Homo sapiens.

XX WO2003080795-A2.
 XX 02-OCT-2003.
 XX 09-AUG-2002; 2003WO-US025485.
 XX 09-AUG-2001; 2001US-0311261P.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Yang Y, Wang Z, Weng G, Ma Y;
 XX WPI; 2003-876918/A1.
 XX N-PSDB; ADF58395.
 XX New polynucleotides, useful as hybridization probes, oligomers or
 XX primers, for chromosome or gene mapping, for the recombinant production
 XX of proteins, and for generating antisense DNA or RNA.
 XX Claim 20; SEQ ID NO 1803; 571pp; English.
 XX The present sequence represents a polypeptide (II) with biological
 XX activity, which is encoded by an isolated polynucleotide sequence (I)
 XX from the present invention. Also described: (1) a vector comprising (I);
 XX (2) an expression vector comprising (I); (3) a host cell genetically
 XX engineered to comprise (I) which is operatively associated with a
 XX regulatory sequence that modulates expression of (I) in the host cell;
 XX (4) a polypeptide (II) encoded by (I); (5) a composition comprising the
 XX polypeptide of (4) and a carrier; (6) an antibody directed against the
 XX polypeptide of (4); (7) detecting (I) or the polypeptide of (4) in a
 XX sample; (8) identifying a compound that binds to the polypeptide of (4);
 XX (9) producing the polypeptide of (4); and (10) a collection of
 XX polynucleotides comprising at least one of the polynucleotide sequences
 XX (I). The polynucleotides (I) can be used as hybridisation probes,
 XX oligomers or primers, for chromosome or gene mapping, for the recombinant
 XX production of proteins, and for generating antisense DNA or RNA.
 XX Sequence 171 AA;
 Alignment Scores:
 Pred. No.: 6.37e-35 Length: 171
 Score: 375.00 Matches: 67
 Percent Similarity: 77.0% Conservative: 0
 Best Local Similarity: 77.0% Mismatches: 2
 Query Match: 74.7% Indels: 18
 DB: 7 Gaps: 1
 US-10-079-954-2 (1-261) x ADF59395 (1-171)
 QY 1 AGCCAGCAACGACGAGGGTGACATAGAGTGTGGTGTCTGTCATGTCGAGAGAGAAAC 60
 Db 31 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 50
 QY 61 ACTTTCGAGTCCAGAACCCAGGAGGTGCAATAGGACAGAGCCATCTGGTGTATAGCG 120
 Db 51 ThrPheGluCysGlnAsnProArgArgCysIleTrpThrGluProTyrCysValIleAla 70
 QY 121 GCCGTGAAAATATTTCCACGTTTTTTCATGTTTCCGCAACAGGTGCTCGCTGGTTGTGCA 180
 Db 71 AlaVal-----Met----- 72
 QY 181 CGCATGGAGAGACCCAGAGAGAGAGCGGTTTCTCTCGGAGAGCCCATGCCCTTC 240
 Db 73 ThrMetGluArgProLysProGluGlyArgPheLeuLeuGluGluProMetProPhe 92
 QY 241 TTTTACCTCAAGTGTGTGAAA 261
 Db 93 PheTyrLeuLysCysCysLys 99
 RESULT 13
 ADS11037
 ID ADS11037 standard; protein; 162 AA.

XX ADS11037;
 XX AC 16-DEC-2004 (first entry)
 XX DT Human therapeutic protein - SEQ ID 1274.
 XX DE antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;
 XX KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
 XX KW aplastic anaemia; cancer; wound healing; gene therapy.
 XX OS Homo sapiens.
 XX WO2004080148-A2.
 XX FN 23-SEP-2004.
 XX PD 30-SEP-2003; 2003WO-US030720.
 XX PF 02-OCT-2002; 2002US-0416186P.
 XX PR (NUVE-) NUVELO INC.
 XX PA Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
 XX PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
 XX PT WPI; 2004-668857/65.
 XX DR N-PSDB; ADS10353.
 XX New polynucleotide, useful in preparing a composition for diagnosing or
 XX treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
 XX aplastic anemia or cancer for promoting wound healing.
 XX Claim 20; SEQ ID NO 1274; 718pp; English.
 XX The invention relates to a novel isolated polynucleotide and the encoded
 XX polypeptide. The molecules of the invention demonstrate antiinflammatory,
 XX neuroprotective, antianaemic, cytostatic and vulnery activities and may
 XX be useful in preparing a composition for diagnosing or treating
 XX inflammatory, haematopoietic, immune, neurodegenerative or stem cell
 XX disorders, such as aplastic anaemia or cancer, as well as for promoting
 XX wound healing. The molecules may also be utilised during gene therapy
 XX procedures. The current sequence is that of a human therapeutic protein
 XX of the invention. The current sequence is not shown explicitly within the
 XX specification but can be accessed from the WIPO web-site.
 XX SQ Sequence 162 AA;
 Alignment Scores:
 Pred. No.: 1.62e-34 Length: 162
 Score: 371.50 Matches: 72
 Percent Similarity: 82.8% Conservative: 0
 Best Local Similarity: 82.8% Mismatches: 2
 Query Match: 74.0% Indels: 13
 DB: 8 Gaps: 1
 US-10-079-954-2 (1-261) x ADS11037 (1-162)
 QY 1 AGCCAGCAACGACGAGGGTGACATAGAGTGTGGTGTCTGTCATGTCGAGAGAGAAAC 60
 Db 89 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 108
 QY 61 ACTTTCGAGTCCAGAACCCAGGAGGTGCAATAGGACAGAGCCATCTGGTGTATAGCG 120
 Db 109 ThrPheGluCysGlnAsnProArgArgCysIleTrpThrGluProTyrCysValIleAla 128
 QY 121 GCCGTGAAAATATTTCCACGTTTTTTCATGTTTCCGCAACAGGTGCTCGCTGGTTGTGCA 180
 Db 129 AlaVal-----Met-----LeuArgTrpLeuCys 137
 QY 181 CGCATGGAGAGACCCAGAGAGAGAGCGGTTTCTCTCGGAGAGCCCATGCCCTTC 240
 Db 137 erAspGlyGluThrGlnAlaArgGlyGluAlaValSerProGlyArgAlaHisAlaLeu 157

QY 145 TTCAAGTTCGCAACAGGTGCTCCGCTGCTGTGTCAGCG-----ATG 186
Db 59 PheTyrValSerLysGlnCysThrArgCysProThrProValValSerProProSer 78
QY 187 GAGACACCAAGCAGAGAGAGCGGTTCTCTGGAAGAGCCCATGCCCTTCTTTTAC 246
Db 79 ThrAsnProProSerGluProLysGluPheLeuIleGluLysProMetProPheLeuPhe 98
QY 247 CTCAGAGTGTGAAA 261
Db 99 TyrLysCysGln 103

Search completed: March 23, 2006, 12:39:56
Job time : 100.355 secs

RESULT 15

AAW36523
ID AAW36523 standard; protein; 158 AA.

XX AC AAW36523;

XX DT 27-MAR-1998 (first entry)

XX DE GPI anchor molecule like protein.

XX KW GPI anchor molecule like protein; GML; wild type p53; diagnosis; cancer.

XX OS Homo sapiens.

XX PN JP09275983-A.

XX PD 28-OCT-1997.

XX PF 15-APR-1996; 96JP-00092559.

XX PR 15-APR-1996; 96JP-00092559.

XX PA (EISA) EISAI CO LTD.

XX DR WPI; 1998-022162/03.

XX DR N-PSDB; AAT96729.

XX PT Protein GML, a target for the p53 protein - useful for diagnosing cancer.

XX PS Claim 1; Page 8-9; 10pp; Japanese.

XX CC This sequence is a GPI anchor molecule like protein (GML). GML gene expression is induced by wild type p53. GML mRNA is expressed in normal tissue and a gullet cancer cell strain. The GML gene can be used to determine p53 function, which is useful for diagnosing cancer

XX SQ Sequence 158 AA;

Alignment Scores:

Pred. No.:	0.0247	Length:	158
Score:	97.50	Matches:	23
Percent Similarity:	46.2%	Conservative:	13
Best Local Similarity:	29.5%	Mismatches:	35
Query Match:	19.4%	Indels:	7
DB:	2	Gaps:	2

US-10-079-954-2 (1-261) x AAW36523 (1-158)

QY 37 TGTCAATGCTGTGAGAGAGAAACACTTTCGAGTGCCAGAACCCAGGAGGTGCAATGG 96

Db 31 CysHisAspCysAlaValIleAsnAspPheAsnCysProAsnIleArgValCysProTyr 50

QY 97 ACAGAGCCATCTGGTGTATAGCGCCGCGTAAATATTTCCACGTTTTTTCATGTTGCGC 156

Db 51 HisIleArgArgCysMetThrIleSerIleArgIleAsnSerArgGluLeuValTyr 70

QY 157 AACAGGTGCTCGCTGGTTGT-----GCAGCGATGGAGAGACCCCAAGCCAGAG 204

Db 71 LysAsnCysThrAsnAsnCysThrPheValTyrAlaAlaGluGlnProProGluAlaPro 90

THIS PAGE BLANK (USPTO)

QY 61 ACTTTCGAGTCCAGAACCCAGAGGTGCAAAATGGACAGACCATCTCGCTTATAGCG 120
Db ThrPheGluCysGlnAsnProArgCysIleYsrThrGluProTyrCysValileAala 67
QY 121 GCGGTGAAATATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTGCA 180
Db AlaVallyIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAala 87
QY 181 GCGATGGAGACCCAGCCAGAGAGAGCGGTTTCTCTCGAAGAGCCCATGCCCTTC 240
Db AlaMetGluA-gProLysProGluGluLysArgPheLeuLeuGluGluProMetProphe 107
QY 241 TTTTACCTCAAGTGTGTAAA 261
Db 108 PheTyrLeuLysCysCysLys 114

RESULT 2

US-10-295-027-754

; Sequence 754, Application US/10295027
; Publication No. US20030232350A1

GENERAL INFORMATION:

; APPLICANT: Afar, Daniel

; APPLICANT: Aziz, Natasha

; APPLICANT: Ginsberg, Wendy M.

; APPLICANT: Gish, Kurt C.

; APPLICANT: Glynn, Richard

; APPLICANT: Hevezi, Peter A.

; APPLICANT: Mack, David H.

; APPLICANT: Murray, Richard

; APPLICANT: Watson, Susan R.

; APPLICANT: Eos Biotechnology, Inc.

; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer

; FILE REFERENCE: 018501-012500US

; CURRENT APPLICATION NUMBER: US/10/295,027

; CURRENT FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: US 09/663,733

; PRIOR FILING DATE: 2000-09-15

; PRIOR APPLICATION NUMBER: US 60/350,666

; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 60/335,394

; PRIOR FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: US 60/332,464

; PRIOR FILING DATE: 2001-11-21

; PRIOR APPLICATION NUMBER: US 60/334,393

; PRIOR FILING DATE: 2001-11-29

; PRIOR APPLICATION NUMBER: US 60/340,376

; PRIOR FILING DATE: 2001-12-14

; PRIOR APPLICATION NUMBER: US 60/347,211

; PRIOR FILING DATE: 2002-01-08

; PRIOR APPLICATION NUMBER: US 60/347,349

; PRIOR FILING DATE: 2002-01-10

; PRIOR APPLICATION NUMBER: US 60/355,250

; PRIOR FILING DATE: 2002-02-08

; PRIOR APPLICATION NUMBER: US 60/356,714

; PRIOR FILING DATE: 2002-02-13

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1386

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 754

; TYPE: PRT

; LENGTH: 165

; ORGANISM: Homo sapiens

US-10-295-027-754

Alignment Scores:

Pred. No.:	2,198-50	Length:	165
Score:	482.00	Matches:	83
Percent Similarity:	96.6%	Conservative:	1
Best Local Similarity:	95.4%	Mismatches:	3
Query Match:	96.0%	Indels:	0
DB:	4	Gaps:	0

US-10-079-954-2 (1-261) x US-10-295-027-754 (1-165)
QY 1 AGCCAGCGAACCGACGAGGTGCAATAGAGTGTGGTGTCTGTTGAGAGAGAAAC 60
Db 31 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 50
QY 61 ACTTTCGAGTCCAGAACCCAGAGGTGCAAAATGGACAGACCATCTCGCTTATAGCG 120
Db 51 ThrPheGluCysGlnAsnProArgCysIleYsrThrGluProTyrCysValileAala 70
QY 121 GCGGTGAAATATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTGCA 180
Db 71 AlaVallyIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAala 90
QY 181 GCGATGGAGACCCAGCCAGAGAGAGCGGTTTCTCTCGAAGAGCCCATGCCCTTC 240
Db 91 AlaMetGluA-gProLysProGluGluLysArgPheLeuLeuGluGluProMetProphe 110
QY 241 TTTTACCTCAAGTGTGTAAA 261
Db 111 PheTyrLeuLysCysCysLys 117

RESULT 3

US-09-977-801-2

; Sequence 2, Application US/09977801

; Publication No. US20020086848A1

GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Fanconi-gene II

; NUMBER OF SEQUENCES: 2

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/977,801

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/402,632

; FILING DATE:

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 223 amino acids

; TYPE: amino acids

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-977-801-2

Alignment Scores:

Pred. No.:	2,36e-50	Length:	223
Score:	482.00	Matches:	83
Percent Similarity:	96.6%	Conservative:	1
Best Local Similarity:	95.4%	Mismatches:	3
Query Match:	96.0%	Indels:	0
DB:	3	Gaps:	0

US-10-079-954-2 (1-261) x US-09-977-801-2 (1-223)

QY 1 AGCCAGCGAACCGACGAGGTGCAATAGAGTGTGGTGTCTGTTGAGAGAGAAAC 60
Db 89 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 108
QY 61 ACTTTCGAGTCCAGAACCCAGAGGTGCAAAATGGACAGACCATCTCGCTTATAGCG 120
Db 109 ThrPheGluCysGlnAsnProArgCysIleYsrThrGluProTyrCysValileAala 128
QY 121 GCGGTGAAATATTTCCACGTTTTTTCATGTTTCGCAACAGGTGCTCGCTGGTTGTGCA 180
Db 129 AlaVallyIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAala 148
QY 181 GCGATGGAGACCCAGCCAGAGAGAGCGGTTTCTCTCGAAGAGCCCATGCCCTTC 240

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Db 149 AlaMetGluArgProLysProGluGluLysArgPheLeuLeuGluGluProMetProPhe 168
Qy 241 TTTTACCTCAAGTGTGTAAA 261
Db 169 PheTyrLeuLysCysCysLys 175

RESULT 4
US-10-199-448-2
; Sequence 2, Application US/10199448
; Publication No. US20030022958A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Mannheim GmbH
; TITLE OF INVENTION: Fanconi-gene II
; NUMBER OF SEQUENCES: 2
; STREET: Sandhofer Str. 112-132
; CITY: Mannheim
; COUNTRY: Germany
; ZIP: 68305
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/199,448
; FILING DATE: 19-Jul-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/977,801
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/09/402,632
; FILING DATE: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-199-448-2

Alignment Scores:
Pred. No.: 2,36e-50 Length: 223
Score: 482.00 Matches: 83
Percent Similarity: 96.4% Conservative: 1
Best Local Similarity: 95.4% Mismatches: 3
Query Match: 96.0% Indels: 0
DB: 4 Gaps: 0

US-10-079-954-2 (1-261) x US-10-199-448-2 (1-223)
Qy 1 AGCCAGCGAACGCGAGGGTGACAAATAGAGTGTGTCTCATGCTTGTGAGAGAAAC 60
Db 89 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 108
Qy 61 ACTTTCCAGTCCAGAACCCCAAGAGGTGCAATAGGACAGCCATCTCGTTTATAGCG 120
Db 109 ThrPheGluCysGlnAsnProArgCysLysTrpThrGluProTyrCysValIleAla 128
Qy 121 GCCGTGAAATATTTCACGTTTTTTCATGTTTCGCAACAGGTGCTCCGCTGTTGTGCA 180
Db 129 AlaValIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 148
Qy 181 GCGATGAGAGACCCAGCCAGGAGGAGGAGGTTTCTCTGGAAGAGCCATGCCCTTC 240
Db 149 AlaMetGluArgProLysProGluGluLysArgPheLeuLeuGluGluProMetProPhe 168
Qy 241 TTTTACCTCAAGTGTGTAAA 261
Db 169 PheTyrLeuLysCysCysLys 175

RESULT 5
US-10-295-027-340
```

```
; Sequence 340, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 340
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-295-027-340

Alignment Scores:
Pred. No.: 2,36e-50 Length: 223
Score: 482.00 Matches: 83
Percent Similarity: 96.6% Conservative: 1
Best Local Similarity: 95.4% Mismatches: 3
Query Match: 96.0% Indels: 0
DB: 4 Gaps: 0

US-10-079-954-2 (1-261) x US-10-295-027-340 (1-223)
Qy 1 AGCCAGCGAACGCGAGGGTGACAAATAGAGTGTGTCTCATGCTTGTGAGAGAAAC 60
Db 89 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 108
Qy 61 ACTTTCCAGTCCAGAACCCCAAGAGGTGCAATAGGACAGCCATCTCGTTTATAGCG 120
Db 109 ThrPheGluCysGlnAsnProArgCysLysTrpThrGluProTyrCysValIleAla 128
Qy 121 GCCGTGAAATATTTCACGTTTTTTCATGTTTCGCAACAGGTGCTCCGCTGTTGTGCA 180
Db 129 AlaValIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 148
Qy 181 GCGATGAGAGACCCAGCCAGGAGGAGGAGGTTTCTCTGGAAGAGCCATGCCCTTC 240
Db 149 AlaMetGluArgProLysProGluGluLysArgPheLeuLeuGluGluProMetProPhe 168
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Qy 241 TTTTACCTCAAGTGTGTA 261
 Db 169 PheTyrLeuLysCysCysLys 175

RESULT 6

US-10-188-832-173
 ; Sequence 173, Application US/10188832
 ; Publication No. US20040076955A1
 ; GENERAL INFORMATION:

APPLICANT: Mack, David H.

APPLICANT: Aziz, Natasha

APPLICANT: Eos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions

and Methods of Screening for Modulators of Bladder

TITLE OF INVENTION: Cancer

FILE REFERENCE: 018501-002330US

CURRENT APPLICATION NUMBER: US/10/188,832

CURRENT FILING DATE: 2002-11-22

PRIOR APPLICATION NUMBER: US 60/302,814

PRIOR FILING DATE: 2001-07-03

PRIOR APPLICATION NUMBER: US 60/310,099

PRIOR FILING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: US 60/343,705

PRIOR FILING DATE: 2001-11-08

PRIOR APPLICATION NUMBER: US 60/350,666

PRIOR FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: US 60/372,246

PRIOR FILING DATE: 2002-04-12

NUMBER OF SEQ ID NOS: 207

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 173

LENGTH: 223

TYPE: PRT

ORGANISM: Homo sapiens

US-10-188-832-173

Alignment Scores:
 Pred. No.: 2,368-50 Length: 223
 Score: 482.00 Matches: 83
 Percent Similarity: 96.6% Conservative: 1
 Best Local Similarity: 95.4% Mismatches: 3
 Query Match: 96.0% Indels: 0
 DB: 4 Gaps: 0

US-10-079-954-2 (1-261) x US-10-188-832-173 (1-223)

Qy 1 AGCCAGCGAAGCGAGGTCACAAATAGAGTGTGTGTCATGCTGTGAGAGAGAAAC 60
 Db 89 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 108
 Qy 61 ACTTTCGAGTGCAGAACCCAGAGGTCGAAATGGACAGAGCCATCTGCGTTATAGCG 120
 Db 109 ThrPheGluCysGlnAsnProArgCysLysTrpThrGluProTyrCysValIleAla 128
 Qy 121 GCCGTGAATAATTTCCACGTTTTTCATGTTTCGCAACAGTGCTCCGCTGGTGTGCA 180
 Db 129 AlaValLysIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 148
 Qy 181 GCGATGGAGAGACCCAGCGAGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTC 240
 Db 149 AlaMetGluArgProLysProGluGluLysArgPheLeuLeuGluGluProMetProphe 168
 Qy 241 TTTTACCTCAAGTGTGTA 261
 Db 169 PheTyrLeuLysCysCysLys 175

RESULT 7

US-11-061-694-4
 ; Sequence 4, Application US/11061694
 ; Publication No. US20050186610A1
 ; GENERAL INFORMATION:

APPLICANT: Samsung Electronics Co. LTD.

TITLE OF INVENTION: Breast cancer cell related protein, a gene encoding the same,

TITLE OF INVENTION: and a method for diagnosing a breast cancer using the protein and
 TITLE OF INVENTION: gene
 FILE REFERENCE: PNO60423
 CURRENT APPLICATION NUMBER: US/11/061,694
 CURRENT FILING DATE: 2005-02-18
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: KopatentIn 1.71
 SEQ ID NO 4
 LENGTH: 223
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-061-694-4

Alignment Scores:
 Pred. No.: 2,368-50 Length: 223
 Score: 482.00 Matches: 83
 Percent Similarity: 96.6% Conservative: 1
 Best Local Similarity: 95.4% Mismatches: 3
 Query Match: 96.0% Indels: 0
 DB: 6 Gaps: 0

US-10-079-954-2 (1-261) x US-11-061-694-4 (1-223)

Qy 1 AGCCAGCGAAGCGAGGTCACAAATAGAGTGTGTGTCATGCTGTGAGAGAGAAAC 60
 Db 89 SerGlnArgThrAspGluGlyAspAsnArgValTrpCysHisValCysGluArgGluAsn 108
 Qy 61 ACTTTCGAGTGCAGAACCCAGAGGTCGAAATGGACAGAGCCATCTGCGTTATAGCG 120
 Db 109 ThrPheGluCysGlnAsnProArgCysLysTrpThrGluProTyrCysValIleAla 128
 Qy 121 GCCGTGAATAATTTCCACGTTTTTCATGTTTCGCAACAGTGCTCCGCTGGTGTGCA 180
 Db 129 AlaValLysIlePheProArgPheMetValAlaLysGlnCysSerAlaGlyCysAla 148
 Qy 181 GCGATGGAGAGACCCAGCGAGAGAGCGGTTTTCTCTGGAAGAGCCCATGCCCTTC 240
 Db 149 AlaMetGluArgProLysProGluGluLysArgPheLeuLeuGluGluProMetProphe 168
 Qy 241 TTTTACCTCAAGTGTGTA 261
 Db 169 PheTyrLeuLysCysCysLys 175

RESULT 8

US-10-072-012-606

Sequence 606, Application US/10072012

Publication No. US20040033493A1

GENERAL INFORMATION:

APPLICANT: Tchevnev, Velizar

APPLICANT: Spytek, Kimberly

APPLICANT: Zerhusen, Bryan

APPLICANT: Patturajan, Meera

APPLICANT: Shimkets, Richard

APPLICANT: Li, Li

APPLICANT: Gangolli, Esha

APPLICANT: Padigaru, Muralidhara

APPLICANT: Anderson, David W.

APPLICANT: Rastelli, Luca

APPLICANT: Miller, Charles E.

APPLICANT: Gerlach, Valerie

APPLICANT: Taupier Jr, Raymond J.

APPLICANT: Gusev, Vladimir Y.

APPLICANT: Colman, Steven D.

APPLICANT: Wolenc, Adam R.

APPLICANT: Pena, Carol E. A

APPLICANT: Furtak, Katarzyna

APPLICANT: Grosse, William M.

APPLICANT: Alsbrook II, John P.

APPLICANT: Lepley, Denise M.

APPLICANT: Rieger, Daniel K.

APPLICANT: Burgess, Catherine E.

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-258

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; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 606
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-072-012-606

Alignment Scores:
Pred. No.: 4,24e-16 Length: 154
Score: 205.00 Matches: 33
Percent Similarity: 57.6% Conservative: 16
Best Local Similarity: 38.8% Mismatches: 30
Query Match: 40.8% Indels: 6
DB: 4 Gaps: 1

US-10-079-954-2 (1-261) x US-10-072-012-606 (1-154)
Qy 25 AATGAGTGGTGTCTGATGAGAGAGAAACACTTTCGAGTGCCAGAACCCAGG 84
Db 19 AsnAlaLeuThrCysHisValCysGluAlaGlnAsnSerTyrAlaCysSerAsnProSer 38
Qy 85 AGGTGCAATGCAGACAGCCACTACTGCGTTATAGCGCGCGTGAATAATTTCCACGTTT 144
Db 39 GlnCysProGlyGluLysLysPheCysLeuLeuAlaValThrArgIlePheGluArgPhe 58
Qy 145 TTCATGGTTCGAACAGGTGCTCCGCTGGTTGTGCAGCG-----ATG 186
Db 59 PheTyrValSerLysGlnCysThrArgArgCysProThrProValValSerProProSer 78
Qy 187 GAGACACCCAGCCAGGAGAGAGCGGTTCTCTGAGAGCCGATGCCCTTTCTTTTAC 246
Db 79 ThrAsnProProSerGluProLysGluPheLeuIleGluLysProMetProPheLeuPhe 98
Qy 247 CTCAGTGTCTGTA 261
Db 99 TyrLysCysGln 103

RESULT 9
US-10-369-493-3710
; Sequence 3710, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3710
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Neurospora crassa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(240)
; OTHER INFORMATION: unsure at all xaa locations
US-10-369-493-3710

Alignment Scores:
Pred. No.: 1.06 Length: 240
Score: 81.00 Matches: 18
Percent Similarity: 47.2% Conservative: 7
Best Local Similarity: 34.0% Mismatches: 20
Query Match: 16.1% Indels: 8
DB: 4 Gaps: 2

US-10-079-954-2 (1-261) x US-10-369-493-3710 (1-240)
Qy 1 AGCCAGCGAACGACGAGGCGTGACATAGAGTGGTGTCTGCTGTGAGAGAGAAAC 60
Db 179 SerGlnHisThrAspProThrAsnGlnArgIleTyrValTyrSerThrGln----- 195
Qy 61 ACTTTCGAGTGCCAGAACCCAGGAGGTGCAATAGGACAGAGCCACTACTCGTTTATAGCG 120
Db 196 -----GluAsnPro---SerAlaProTyrLysGluMetTyrCysPheAlaAla 210
Qy 121 GCCGTGAAATATTTCCACGTTTTTTCATCGTTCGCGAAC 159
Db 211 AspThrGluPhePheProAlaAspPheGluValMetAsn 223

RESULT 10
US-10-282-122A-61811
; Sequence 61811, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
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; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 61811
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Mycobacterium avium
US-10-282-122A-61811

Alignment Scores:
Pred. No.: 1.76 Length: 583
Score: 80.00 Matches: 21
Percent Similarity: 43.7% Conservative: 10
Best Local Similarity: 29.6% Mismatches: 30
Query Match: 15.9% Indels: 10
DB: 4 Gaps: 1

US-10-079-954-2 (1-261) x US-10-282-122A-61811 (1-583)
QY 66 CGAGTGCAGACCCCAAGGAG-----GTGCAATG 95
Db 294 ArgValHisGluProHisGluThrValArgIleAlaLeuValGlyLysTyrValGluLeu 313
QY 96 GACAGGCACTATCGTGTATAGCGCGGTGAAATATTTCCACGTTTTTTCATGGTTCG 155
Db 314 SerAspAlaTyrLeuSerValThrGluAlaLeuArgAlaGlyPhePheHisAla 333
QY 156 CAACAGGTGCTCCGCTGTGTGTCAGCGATGAGACCCCAAGCGAGAGAGCGGTT 215
Db 334 LysValGluMetValTyrValAlaSerAspAspCysGluSerAlaSerGlyAlaAla 353
QY 216 TCTCTCGAAGACCCCATCGCTTCTTTTACT 248
Db 354 AlaLeuGlyGluValHisGlyValLeuIlePro 364

RESULT 11
US-10-437-963-174792
; Sequence 174792, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 174792
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_726C.1.pep
US-10-437-963-174792

Alignment Scores:
Pred. No.: 2.36 Length: 106
Score: 77.50 Matches: 23
Percent Similarity: 39.2% Conservative: 6
Best Local Similarity: 31.1% Mismatches: 30
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Query Match: 15.4% Indels: 15
DB: 4 Gaps: 4

US-10-079-954-2 (1-261) x US-10-437-963-174792 (1-106)
QY 40 CATGCTGTGAGAGAGAAACACTTTCGAGTGCAGAACCCA----- 81
Db 24 HisArgCysHisArgHisArgGlyTyrArgLeuGluGlnProGlyGlnAsnHisAlaLeu 43
QY 82 -----AGGAGGTGCAATGACAGACAGACCCATCTGCTTATAGCGCGGTGAAA--- 129
Db 44 CysSerGlyGlyArgCysGlnTyrArgTyrArgHisCysValGlnAlaAlaThrSerPro 63
QY 130 ATATTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGTTGTCGAGCGATGAG 189
Db 64 LeuLeuProArgAlaPheSer---ArgSerArgMetLeuGlyAlaAlaThrAlaProPro 82
QY 190 AGACCCCAAGCAGAGGAGAGCGGTTTCTCTCGAAGAGGCC 231
Db 83 ArgProProAlaArg-----TyrGluGluPro 92

RESULT 12
US-10-282-122A-45313
; Sequence 45313, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 45313
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (151)..(151)
; OTHER INFORMATION: X=any amino acid
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FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (280)..(280)
OTHER INFORMATION: X=any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (302)..(302)
OTHER INFORMATION: X=any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (561)..(561)
OTHER INFORMATION: X=any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (620)..(620)
OTHER INFORMATION: X=any amino acid
US-10-282-122A-45313
Alignment Scores:
Pred. No.: 7.47 Length: 636
Score: 75.00 Matches: 27
Percent Similarity: 48.8% Conservative: 14
Best Local Similarity: 32.1% Mismatches: 32
Query Match: 14.9% Indels: 11
DB: 4 Gaps: 2
US-10-079-954-2 (1-261) x US-10-282-122A-45313 (1-636)
Qy 254 CACTGTGAGTAAAGAGGCGATGGCTCTCCAGGAGAACCCCTCTCTCTGGCTTG 195
Db 93 HisalagGlyLysPheGlyGlnGlyGlyTyrLysThrSerGlyGlyLeuHisGlyVal 112
Qy 194 GGTCTCTCATCGCTGCACACACGCGGACCTGTTGCGAACCATGAAACGTTGGA 135
Db 113 GlylaserValvalasnAlaLeuSerGluTrpLeuValThrIleLysArgAspGly 132
Qy 134 AATATTTTCAGCGCGCTATACACGATGCTCTGTCCATTTCACCTCTCTGGT-- 77
Db 133 AsnileTyrGluHisAlaLeuLeuGlyGly-ValproValThrSerLeu**Ly 152
Qy 76 -----TCTGCACCTCGAAGTGTCTCTCTCTCACAGCATGACAC 36
Db 152 sileGlyLysThrLysGluSerGlyThrThrMetHisPhe-----LysProAspTh 169
Qy 35 CACACTCTAT 26
Db 169 rThrilephe 172
RESULT 13
US-10-437-963-124768
Sequence 124768, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 124768
LENGTH: 326
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_27475C.1.pep
US-10-437-963-124768
Alignment Scores:
Pred. No.: 11.2 Length: 326
Score: 73.00 Matches: 12
Percent Similarity: 71.4% Conservative: 8
Best Local Similarity: 42.9% Mismatches: 8
Query Match: 14.5% Indels: 0
DB: 4 Gaps: 0
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Qy 167 GAGCACCTGTTCGGAACCATGAAACCGTGGAAATATTTTCACGCGCTATAACGAG 108
Db 188 GlnSerLeuValAspArgLeuLysAsnValGlyAspLeuLeuThrValAlaValThrGln 207
Qy 107 TATGGCTCTGTCCATTTCGACCTC 84
Db 208 TyrGlyAspLeuHisLeuHisVal 215
RESULT 14
US-09-746-783-218
Sequence 218, Application US/09746783
Publication No. US20030044935A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallie, Edward R.
APPLICANT: Racine, Lisa A.
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Pechtel, Kim
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/746,783
FILING DATE: 21-Dec-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Milasincic, Debra J.
REGISTRATION NUMBER: 46,931
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 218:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-09-746-783-218
Alignment Scores:
Pred. No.: 13.1 Length: 342
Score: 72.50 Matches: 24
Percent Similarity: 45.0% Conservative: 12
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```
Best Local Similarity: 30.0%      Mismatches: 29
Query Match:      14.4%      Indels: 15
DB:              3          Gaps: 4

US-10-079-954-2 (1-261) x US-09-746-783-218 (1-342)

Qy 22 GACATAGAGTGTGGTGCATGCTGTGAGAGAGAAACACTTTCGAGTCCAGAACCCA 81
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Db 69 AspArgAlaValLeuIleSerAlaCysGluArg-----GlyCysArgLeuPhe 84
   |||
Qy 82 AGGAGGTGCAATGG-----ACAGAGCCCATACTGCGTT 114
   |||
Db 85 SerIleCysArgPheValAlaArgSerSerLysProAsnAlaThrGlnThrGluCysGlu 104
   |||
Qy 115 ATAGCGGCGGTGAAATATTTCCAGTGTTCATGTTTCGCAACAGGTGCTCCGCTGGT 174
   |||
Db 105 AlaAlaCysValGluAlaTyValLys---GluAlaGluGlnGlnAlaCysSerHisGly 123
   |||
Qy 175 TGT---GCAGCGATGGAGAGACCCAGCCAGCAGGAGAGCGGTTTCTCTGGAAGAGCCC 231
   |||
Db 124 CysTrpSerGlnProAlaGluProGluProGluGlnLysArgLysValLeuGluAlaPro 143

RESULT 15
US-10-296-115-1297
; Sequence 1297, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296.115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1297
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-296-115-1297

Alignment Scores:
Pred. No.: 13.2      Length: 353
Score: 72.50      Matches: 24
Percent Similarity: 45.0%      Conservative: 12
Best Local Similarity: 30.0%      Mismatches: 29
Query Match: 14.4%      Indels: 15
DB: 4          Gaps: 4

US-10-079-954-2 (1-261) x US-10-296-115-1297 (1-353)

Qy 22 GACATAGAGTGTGGTGCATGCTGTGAGAGAGAAACACTTTCGAGTCCAGAACCCA 81
   |||
Db 80 AspArgAlaValLeuIleSerAlaCysGluArg-----GlyCysArgLeuPhe 95
   |||
Qy 82 AGGAGGTGCAATGG-----ACAGAGCCCATACTGCGTT 114
   |||
Db 96 SerIleCysArgPheValAlaArgSerSerLysProAsnAlaThrGlnThrGluCysGlu 115
   |||
Qy 115 ATAGCGGCGGTGAAATATTTCCAGTGTTCATGTTTCGCAACAGGTGCTCCGCTGGT 174
   |||
Db 116 AlaAlaCysValGluAlaTyValLys---GluAlaGluGlnGlnAlaCysSerHisGly 134
   |||
Qy 175 TGT---GCAGCGATGGAGAGACCCAGCCAGCAGGAGAGCGGTTTCTCTGGAAGAGCCC 231
   |||
Db 135 CysTrpSerGlnProAlaGluProGluProGluGlnLysArgLysValLeuGluAlaPro 154
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Search completed: March 23, 2006, 12:54:45
Job time : 80.5807 secs

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:49:19 ; Search time 2.15161 Seconds
(without alignments)
694.416 Million cell updates/sec

Title: US-10-079-954-2

Perfect score: 502

Sequence: 1 agccaggaagcggagcggg.....tttacctcaagtgtgtgaaa 261

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 339260

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q=/abss/ABSSWEB_gpool/US10079934/runat_23032006_102937_1988/app_query.fasta_1
-DB=Published Applications_AA New -QFMT=fastan -SUFFIX=rapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02p
-USER=US10079934@CGN_1_1_24 @runat_23032006_102937_1988 -NCPU=6 -ICPU=3
-NO MMAP -NEG_SCORES=0 -WAIT -DSFLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications_AA New:
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72.5	14.4	342	6	US-10-689-742-218
2	68	13.5	1476	6	US-10-647-956A-4
3	66.5	13.2	178	6	US-10-892-379-4
C 4	66	13.1	366	6	US-10-055-877-302
C 5	66	13.1	469	6	US-10-063-703-58
C 6	66	13.1	469	7	US-11-102-240-58
C 7	66	13.1	469	7	US-11-103-195-58
8	66	13.1	906	7	US-11-124-635-4
9	66	13.1	934	7	US-11-077-386-17

10	66	13.1	1390	6	US-10-957-351-1	Sequence 1, Appli
11	66	13.1	1408	7	US-11-072-175-186	Sequence 186, App
12	65.5	13.0	618	7	US-11-078-735-18	Sequence 18, Appl
13	65.5	13.0	618	7	US-11-050-346-63	Sequence 63, Appl
14	65.5	13.0	618	7	US-11-103-077-18	Sequence 18, Appl
C 15	65	12.9	430	7	US-11-087-099-12253	Sequence 12253, A
16	65	12.9	858	6	US-10-878-556A-113	Sequence 113, App
17	64.5	12.8	73	5	US-09-978-360A-578	Sequence 578, App
18	64	12.7	169	7	US-11-096-568A-12447	Sequence 12447, A
19	64	12.7	174	7	US-11-096-568A-12446	Sequence 12446, A
C 20	64	12.7	350	7	US-11-087-099-2497	Sequence 2497, Ap
C 21	64	12.7	350	7	US-11-087-099-11952	Sequence 11952, A
22	63.5	12.6	533	6	US-10-467-657-8	Sequence 8, Appli
23	63.5	12.6	567	6	US-10-467-657-4328	Sequence 4328, Ap
24	63.5	12.6	1379	7	US-11-114-962-4	Sequence 4, Appli
25	63	12.5	166	7	US-11-176-830-255	Sequence 255, App
C 26	63	12.5	517	7	US-11-037-243-76	Sequence 76, Appl
C 27	63	12.5	1074	7	US-11-087-099-1585	Sequence 1585, Ap
28	62.5	12.5	757	6	US-10-055-877-190	Sequence 190, App
29	62	12.4	166	7	US-11-176-830-1198	Sequence 1198, Ap
30	62	12.4	166	7	US-11-196-067-394	Sequence 394, App
C 31	62	12.4	756	6	US-10-055-877-34	Sequence 34, Appl
C 32	62	12.4	756	6	US-10-055-877-187	Sequence 187, App
C 33	62	12.4	756	6	US-10-055-877-188	Sequence 188, App
C 34	62	12.4	756	6	US-10-055-877-189	Sequence 189, App
C 35	62	12.4	830	6	US-10-055-877-32	Sequence 32, Appl
C 36	61.5	12.3	196	6	US-10-967-527A-27	Sequence 27, Appl
37	61.5	12.3	323	7	US-11-240-769-103	Sequence 103, App
C 38	61	12.2	60	5	US-09-978-360A-592	Sequence 592, App
C 39	61	12.2	181	7	US-11-096-568A-27033	Sequence 27033, A
C 40	60.5	12.1	337	7	US-11-096-568A-7804	Sequence 7804, Ap
C 41	60.5	12.1	342	7	US-11-096-568A-7803	Sequence 7803, Ap
C 42	60.5	12.1	501	7	US-11-096-568A-7802	Sequence 7802, Ap
C 43	60.5	12.1	960	7	US-11-169-041-177	Sequence 177, App
C 44	60	12.0	86	7	US-11-172-536-1	Sequence 1, Appli
45	60	12.0	97	7	US-11-172-536-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-689-742-218
; Sequence 218, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: LaVallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 218
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-218

Alignment Scores:
Pred. No.: 1.44
Score: 72.50
Percent Similarity: 45.0%
Best Local Similarity: 30.0%
Query Match: 14.4%
Matches: 342
Conservative: 24
Mismatches: 12
Indels: 15

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DB:
US-10-079-954-2 (1-261) x US-10-689-742-218 (1-342)
QY 22 GACATAGAGTGGTGTGTCATGCTTGTGAGAGAGAAACACTTTTCGAGTGCAGAACCCA 81
Db 69 AspArgAlaValLeuIleSerAlaCysGluArg-----GlyCysArgLeuPhe 84
QY 82 AGGAGGTCCAATGG-----ACAGAGCCCATCTGCGTT 114
Db 85 SerIleCysArgPheValAlaArgSerSerLysProAenAlaThrGlnThrGluCysGlu 104
QY 115 ATAGCGGCGCGAAATATTTCCAGTGTTCATGGTTCACACAGGTGCTCCGCTGCT 174
Db 105 AlaAlaCysValGluAlaTyrValLys---GluAlaGluGlnGlnAlaCysSerHisGly 123
QY 175 TGT---GCAGCGATGGAGAGACCCCAAGCCAGAGAGAGCGGTTTCTCTCGAAGAGGCC 231
Db 124 CysTrpSerGlnProAlaGluProGluProGluGlnLysArgLysValLeuGluAlaPro 143
RESULT 2
US-10-647-956A-4
; Sequence 4, Application US/10647956A
; Publication No. US20050251878A1
; GENERAL INFORMATION:
; APPLICANT: ffrench-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/10/647,956A
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/817,514
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 1476
; TYPE: PRT
; ORGANISM: Photorhabdus luminescens
US-10-647-956A-4
Alignment Scores:
Pred. No.: 5.37 Length: 1476
Score: 68.00 Matches: 23
Percent Similarity: 42.9% Conservative: 7
Best Local Similarity: 32.9% Mismatches: 22
Query Match: 13.5% Indels: 18
DB: 6 Gaps: 3
US-10-079-954-2 (1-261) x US-10-647-956A-4 (1-1476)
QY 53 GAGAAACACTTTCAGTGCAGAACCCAGAGGTGCAATGACAGAGCCATCTACTCG 112
Db 791 GluGlnThrAspSerHisGlnLeuAlaGlnGlyAenAlaProGluArgThrProAla 810
QY 113 TTATAGCGCGCGTGAATAATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTG 172
Db 811 LeuThrLys-----SerTrpTyrAlaThrGlyLeuProAla 822
QY 173 GTT-----GTGAGCGATGGAGAGACCCCAAGCCAGAGAGAGCGGTTTC 217
Db 823 ValAspAenAlaLeuSerAlaGlyTyrTrpArgGlyAspLysGlnAlaPheAlaGlyPhe 842
QY 218 TCCTGGAGAGCCCATGCGCTCTCTTTTACC 247
Db 843 Thr-----ProArgPheThr 847
RESULT 3
US-10-892-379-4
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```
; Sequence 4, Application US/10892379
; Publication No. US20050282999A9
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Ozenberger, Bradley A.
; APPLICANT: Bard, Jonathan A.
; APPLICANT: Kajkowski, Eileen M.
; APPLICANT: Jacobsen, Jack S.
; APPLICANT: Walker, Stephen G.
; APPLICANT: Sophia, Heidi
; APPLICANT: Howland, David
; TITLE OF INVENTION: Beta-Amyloid Peptide-Binding Proteins and Polynucleotides
; FILE REFERENCE: 31896-67300 (AHP98128P2 Cl)
; CURRENT APPLICATION NUMBER: US/10/892,379
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: 09/852,100
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/774,936
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: US 09/172,990
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: US 09/060,609
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: US 60/064,583
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-892-379-4
Alignment Scores:
Pred. No.: 6.9 Length: 178
Score: 66.50 Matches: 16
Percent Similarity: 42.1% Conservative: 0
Best Local Similarity: 42.1% Mismatches: 17
Query Match: 13.2% Indels: 5
DB: 6 Gaps: 1
US-10-079-954-2 (1-261) x US-10-892-379-4 (1-178)
QY 10 ACGAGAGAGGTGACATAGAGTGTGTCATGCTGTGAGAGAGAAACACTTTTCGAG 69
Db 53 ThrArgGluGlyArgAlaArgValTrpCysIleAlaAlaAenGluIleAenCysThrGlu 72
QY 70 TGCAGAGAACCAAGG-----AGGTGCAATGCGACAGAGCCATAC 108
Db 73 ThrGlyAenAlaThrPheThrArgGluValProCysLysTrpThrAenGlyTyr 90
RESULT 4
US-10-055-877-302
; Sequence 302, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Wei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Rattelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zernusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
```

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; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkete, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 302
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-055-877-302

Alignment Scores:
Pred. No.: 8.32 Length: 366
Score: 66.00 Matches: 17
Percent Similarity: 51.7% Conservative: 14
Best Local Similarity: 28.3% Mismatches: 19
Query Match: 13.1% Indels: 10
DB: 6 Gaps: 3

US-10-079-954-2 (1-261) x US-10-055-877-302 (1-366)
Qy 197 TTGGTCTCTCCATCGTCACACGCGGAGCACCCTGTTGCGAACCATGAAAAACGT 138
Db 7 LeuGlyVallyslleSerGluGlnGlnAlaGlyLeuLeuLeuHisLeuHisProVal 26
Qy 137 GGAATATTTTACGCGCGCTATACGCGATGATGCTCTGTCCATTTG----- 90
Db 27 GlyThrMet---ThrIleAspTrpAsnGluTrpArgAspTyrHisLeuHisProVal 45
Qy 89 -----CACCTCTGGTCTGCG---CACTGAAAGTGTTCCTCTCACA 45
Db 46 GluAsnIleProGluIleLeuTyrTrpLysHisSerThrIlePheAspValGlyGlu 65

RESULT 5
US-10-063-703-58
; Sequence 58, Application US/10063703
; Publication No. US20060008901A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS
; FILE REFERENCE: P3230R1C106C
; CURRENT APPLICATION NUMBER: US/11/102,240
; CURRENT FILING DATE: 2005-04-08
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 199-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 58
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-11-102-240-58
```

```
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,703
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: 10/063662
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 199-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 58
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-063-703-58

Alignment Scores:
Pred. No.: 8.47 Length: 469
Score: 66.00 Matches: 17
Percent Similarity: 51.7% Conservative: 14
Best Local Similarity: 28.3% Mismatches: 19
Query Match: 13.1% Indels: 10
DB: 6 Gaps: 3

US-10-079-954-2 (1-261) x US-10-063-703-58 (1-469)
Qy 197 TTGGTCTCTCCATCGTCACACGCGGAGCACCCTGTTGCGAACCATGAAAAACGT 138
Db 110 LeuGlyVallyslleSerGluGlnGlnAlaGlyLeuLeuLeuHisLeuHisProVal 129
Qy 137 GGAATATTTTACGCGCGCTATACGCGATGATGCTCTGTCCATTTG----- 90
Db 130 GlyThrMet---ThrIleAspTrpAsnGluTrpArgAspTyrHisLeuHisProVal 148
Qy 89 -----CACCTCTGGTCTGCG---CACTGAAAGTGTTCCTCTCACA 45
Db 149 GluAsnIleProGluIleLeuTyrTrpLysHisSerThrIlePheAspValGlyGlu 168

RESULT 6
US-11-102-240-58
; Sequence 58, Application US/11102240
; Publication No. US20050260647A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS
; FILE REFERENCE: P3230R1C106C
; CURRENT APPLICATION NUMBER: US/11/102,240
; CURRENT FILING DATE: 2005-04-08
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 199-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 58
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-11-102-240-58
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Db      540 TrpCysHisAsp-----LysCysValArgSerGluGluCysLeu 555
QY      91 -----AAATGGACAGACCATACTGCCTTATACGCCCGCGTGAAAATAATTTCCACGTTTT 144
Db      553 SerGlyThrTrpThrGlnGlnIleCysLeuProAlaIleTyLysValPheProAsnSer 572
QY      145 TTCATGGTTCGCAACAGACTGCTCGCTGTGTGTCAGCGATGGAGAGACCCCAAGCCAGAG 204
Db      573 AlaProLeuGluGly-GlyThrArgLeuThrIleCysGlyTrpAspPheGlyPheArgAr 592
QY      205 GAGAAGCGGTTTCTCTCTGGAAG 226
Db      592 gAenAsnLysPheAspLeuLys 599

RESULT 11
US-11-072-175-186
; Sequence 186, Application US/11072175
; Publication No. US20060029944A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273A CIP
; CURRENT APPLICATION NUMBER: US/11/072,175
; CURRENT FILING DATE: 2005-03-05
; PRIOR APPLICATION NUMBER: US 60/406,385
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 10/648,593
; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 186
; LENGTH: 1408
; TYPE: PRF
; ORGANISM: Homo sapiens
US-11-072-175-186

Alignment Scores:
Pred. No.:          9.17           Length:         1408
Score:             66.00          Matches:        18
Percent Similarity: 38.2%         Conservative:    8
Best Local Similarity: 26.5%       Mismatches:     31
Query Match:       13.1%          Indels:        11
DB:                7              Gaps:          2

US-10-079-954-2 (1-261) x US-11-072-175-186 (1-1408)
QY      34 TGGTGTGTCATGCTTGTGTGAGAGAGAAACACTTTCGATGCGCACCAAGGAGTGTC--- 90
Db      540 TrpCysHisAsp-----LysCysValArgSerGluGluCysLeu 552
QY      91 -----AAATGGACAGACCATACTGCCTTATACGCCCGCGTGAAAATAATTTCCACGTTTT 144
Db      553 SerGlyThrTrpThrGlnGlnIleCysLeuProAlaIleTyLysValPheProAsnSer 572
QY      145 TTCATGGTTCGCAACAGACTGCTCGCTGTGTGTCAGCGATGGAGAGACCCCAAGCCAGAG 204
Db      573 AlaProLeuGluGly-GlyThrArgLeuThrIleCysGlyTrpAspPheGlyPheArgAr 592
QY      205 GAGAAGCGGTTTCTCTCTGGAAG 226
Db      592 gAenAsnLysPheAspLeuLys 599

RESULT 12
US-11-078-735-18
; Sequence 18, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
```

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS

; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078.735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 18
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-078-735-18

Alignment Scores:
Pred. No.: 9.89 Length: 618
Score: 65.50 Matches: 27
Percent Similarity: 39.8% Conservative: 14
Best Local Similarity: 26.2% Mismatches: 35
Query Match: 13.0% Indels: 27
DB: 7 Gaps: 7

US-10-079-954-2 (1-261) x US-11-078-735-18 (1-618)

Qy 13 GACGAGGTGACAAATAGAGTGTGTCTCATCTCT---TGTGAGAGAGAAAACACTTTTCGAG 69
Db 212 AspGluCysGluAlaProLeuValCysArgAlaGlyCysSerProGluHisGlyPhe--- 230
Qy 70 TGCCAGAACCCAGAGAGAGTGTGCAAA-----TGGACAGAGCCATCTGCGTTATA 117
Db 231 CysGluGlnProGlyGluCysArgCysLeuGluGlyTrpThrGlyProLeuCysThrVal 250
Qy 118 -----GGCGCGTGAAAATATTTCCAGT-----TTTTTC 147
Db 251 ProValSerThrSerSerCysLeuSerProArgGlyProSerSerAlaThrThrGlyCys 270
Qy 148 ATGGTT-----CGCAACAGGTCTCCGCTGTTGTGCGAGCGATG 186
Db 271 LeuValProGlyProGlyProCysAspGlyAsnProCysAlaAsnGlyGlySerCysSer 290
Qy 187 GAGACACCAAGCCAGAGAGAGCGGTTCTCTGGAAGAGCCATGCCCTCTTTTAC 246
Db 291 GluThrPro-----ArgSerPheGluCysThrCysProArgGlyPheGly 306
Qy 247 CTCAGTGT 255
Db 307 LeuArgCys 309

RESULT 13

US-11-050-346-63
; Sequence 63, Application US/11050346
; Publication No. US20060002924A1
; GENERAL INFORMATION:
; APPLICANT: BODMER, MARK WILLIAM
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA

; APPLICANT: WARD, GEORGE ALBERT
; TITLE OF INVENTION: CONJUGATE OF NOTCH SIGNALLING PATHWAY MODULATORS AND
; TITLE OF INVENTION: THEIR USE IN MEDICAL TREATMENT

; FILE REFERENCE: 674525-2016
; CURRENT APPLICATION NUMBER: US/11/050.346
; CURRENT FILING DATE: 2005-02-03
; PRIOR APPLICATION NUMBER: GB 0312062.3
; PRIOR FILING DATE: 2003-05-24
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: GB 0218068.5
; PRIOR FILING DATE: 2002-08-03
; PRIOR APPLICATION NUMBER: GB 0220849.4
; PRIOR FILING DATE: 2002-09-07
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 63
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-050-346-63

Alignment Scores:
Pred. No.: 9.89 Length: 618
Score: 65.50 Matches: 27
Percent Similarity: 39.8% Conservative: 14
Best Local Similarity: 26.2% Mismatches: 35
Query Match: 13.0% Indels: 27
DB: 7 Gaps: 7

US-10-079-954-2 (1-261) x US-11-050-346-63 (1-618)

Qy 13 GACGAGGTGACAAATAGAGTGTGTCTCATCTCT---TGTGAGAGAGAAAACACTTTTCGAG 69
Db 212 AspGluCysGluAlaProLeuValCysArgAlaGlyCysSerProGluHisGlyPhe--- 230
Qy 70 TGCCAGAACCCAGAGAGAGTGTGCAAA-----TGGACAGAGCCATCTGCGTTATA 117
Db 231 CysGluGlnProGlyGluCysArgCysLeuGluGlyTrpThrGlyProLeuCysThrVal 250
Qy 118 -----GGCGCGTGAAAATATTTCCAGT-----TTTTTC 147
Db 251 ProValSerThrSerSerCysLeuSerProArgGlyProSerSerAlaThrThrGlyCys 270
Qy 148 ATGGTT-----CGCAACAGGTCTCCGCTGTTGTGCGAGCGATG 186
Db 271 LeuValProGlyProGlyProCysAspGlyAsnProCysAlaAsnGlyGlySerCysSer 290
Qy 187 GAGACACCAAGCCAGAGAGAGCGGTTCTCTGGAAGAGCCATGCCCTCTTTTAC 246
Db 291 GluThrPro-----ArgSerPheGluCysThrCysProArgGlyPheGly 306
Qy 247 CTCAGTGT 255
Db 307 LeuArgCys 309

RESULT 14

US-11-103-077-18
; Sequence 18, Application US/11103077
; Publication No. US20060003927A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: YOUNG, LESLEY LYNN

;; TITLE OF INVENTION: MODULATION OF IMMUNE FUNCTION

;; FILE REFERENCE: 674525-2020
;; CURRENT APPLICATION NUMBER: US/11/103,077
;; CURRENT FILING DATE: 2005-04-11
;; PRIOR APPLICATION NUMBER: PCT/GB03/04402
;; PRIOR FILING DATE: 2003-10-09
;; PRIOR APPLICATION NUMBER: GB 0223405.2
;; PRIOR FILING DATE: 2002-10-09
;; PRIOR APPLICATION NUMBER: GB 0223409.4
;; PRIOR FILING DATE: 2002-10-09
;; PRIOR APPLICATION NUMBER: GB 0224353.3
;; PRIOR FILING DATE: 2002-10-19
;; NUMBER OF SEQ ID NOS: 29
;; SOFTWARE: PatentIn Ver. 3.3
;; SEQ ID NO 18
;; LENGTH: 618
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-103-077-18

Alignment Scores:
Pred. No.: 9 89 Length: 618
Score: 65.00 Matches: 27
Percent Similarity: 39.8% Conservative: 14
Best Local Similarity: 26.2% Mismatches: 35
Query Match: 13.0% Indels: 27
DB: 7 Gaps: 7

US-10-079-954-2 (1-261) x US-11-103-077-18 (1-618)

Qy 13 GACGAGGTGACAATPAGATGTGGTGCATGCT---TGTGAGAGAGAAAACACTTTTCGAG 69
Db 212 AspGluCysGluAlaProLeuValCysArgAlaGlyCysSerProGluHisGlyPhe--- 230
Qy 70 TCCACAGACCCAGAGAGTGCNAA-----TCGACAGACCCATAGTCGTATATA 117
Db 231 CysGluGlnProGlyGluCysArgCysLeuGluGlyTrpThrGlyProLeuCysThrVal 250
Qy 118 -----GCGGCGGTGAAAATATTTCCACGT-----TTTTTC 147
Db 251 ProValSerThrSerCysLeuSerProArgGlyProSerSerAlaThrThrGlyCys 270
Qy 148 ATGGTT-----CGCAACAGGTCTCCGCTGGTGTGTCAGCGATG 186
Db 271 LeuValProGlyProGlyProCysAspGlyAanProCysAlaAanGlyGlySerCysSer 290
Qy 187 GAGAGACCAAGCCAGAGAGAGCGGTTTCTCTGGAGAGCCCATGCCCTTCTTTTAC 246
Db 291 GluThrPro-----ArgSerPheGluCysThrCysProArgGlyPheTyrgly 306
Qy 247 CTCAGTGT 255
Db 307 LeuArgCys 309

RESULT 15

US-11-087-099-12253
; Sequence 12253, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 12253
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Brassica rapa
US-11-087-099-12253

Alignment Scores:
Pred. No.: 11 Length: 430

Score: 65.00 Matches: 17
Percent Similarity: 46.2% Conservative: 7
Best Local Similarity: 32.7% Mismatches: 22
Query Match: 12.9% Indels: 6
DB: 7 Gaps: 1

US-10-079-954-2 (1-261) x US-11-087-099-12253 (1-430)

Qy 215 AACCGCTTCTCCTCTGGCTTGGTCTCTCCATCGTCGACAAACGCGGAGCAGCCTGTTG 156
Db 25 AsnThrLeuSerSerThrGluSerLeuThrIleSerSerAan----- 38
Qy 155 CGAACCATGAAAAACGTGGAATATTTTCAOGCCGCTATAACGCAGATATGGCTCTGTC 96
Db 39 ArgThrLeuValSerArgGlyAanValPheGluLeuGlyPheArgThrAanSerSer 58
Qy 95 CATTTGCACCTCTTGGTCTTGGCACTCGCAAGTG 60
Db 59 SerArgTrpTyrLeuGlyIleTrpTyrLysVal 70

Search completed: March 23, 2006, 12:55:39
Job time : 14.7581 secs

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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:46:10 ; Search time 4:77097 Seconds
(without alignments)
904.569 Million cell updates/sec

Title: US-10-079-954-2

Perfect score: 502

Sequence: 1 agccagcgaacggcagcggg.....tttaccctcaagtgtgttaa 261

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/abs/ABSSWEB.spool/US10079954/runat 23032006 102933 1875/app_query.fasta_1
-DB=Issued_Patents_AA -QFMT=fastcan -SUFFIX=ra1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abs02p -USRR=US10079954 @CGN 1 1 101 @runat 23032006 102933 1875
-NCPU=6 -ICPU=3 -NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pcp:*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pcp:*
3: /cgn2_6/ptodata/1/iaa/H COMB.pcp:*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp:*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pcp:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97.5	19.4	187	2	US-09-949-016-10507
2	75	14.9	159	2	US-09-252-991A-28542
3	73	14.5	136	2	US-09-252-991A-20192
C 4	71.5	14.2	350	2	US-09-248-736A-17746
C 5	71.5	14.2	589	2	US-09-740-041-2
C 6	69	13.6	441	2	US-09-252-991A-18870
C 7	68.5	13.6	559	2	US-09-364-206-47
C 8	68	13.5	1476	2	US-09-817-514A-4
C 9	67.5	13.4	234	2	US-09-270-767-45485
10	67	13.3	598	2	US-09-540-236-3415
11	66.5	13.2	157	2	US-09-252-991A-30532
12	66.5	13.2	178	2	US-09-852-100B-4

C 13	66	13.1	312	2	US-09-188-930-142	Sequence 142, App
C 14	66	13.1	312	2	US-09-312-283C-142	Sequence 142, App
C 15	66	13.1	358	2	US-09-561-077C-64	Sequence 64, Appl
C 16	66	13.1	429	2	US-09-328-352-4392	Sequence 4392, Ap
C 17	66	13.1	469	2	US-09-188-930-339	Sequence 339, App
C 18	66	13.1	469	2	US-09-312-283C-339	Sequence 339, App
C 19	66	13.1	469	2	US-09-991-181-289	Sequence 289, App
C 20	66	13.1	469	2	US-09-990-444-289	Sequence 289, App
C 21	66	13.1	469	2	US-09-997-333-289	Sequence 289, App
C 22	66	13.1	469	2	US-09-992-598-289	Sequence 289, App
C 23	66	13.1	675	1	US-08-386-495-10	Sequence 10, Appl
C 24	66	13.1	675	4	PCT-US96-02331-10	Sequence 10, Appl
C 25	66	13.1	1214	2	US-10-164-595-24	Sequence 24, Appl
C 26	66	13.1	1441	2	US-09-949-016-10397	Sequence 10397, A
C 27	66	13.1	1481	2	US-09-251-645-14	Sequence 14, Appl
C 28	65	12.9	725	2	US-09-234-332-12	Sequence 12, Appl
C 29	65	12.9	842	2	US-09-949-016-8357	Sequence 8357, Ap
C 30	65	12.9	858	2	US-09-538-092-1127	Sequence 1127, Ap
C 31	64.5	12.8	116	2	US-09-973-278-157	Sequence 157, App
C 32	64.5	12.8	117	2	US-09-227-357-238	Sequence 238, App
C 33	64.5	12.8	137	2	US-09-621-976-5741	Sequence 5741, Ap
C 34	64.5	12.8	859	2	US-09-369-364A-5	Sequence 5, Appli
C 35	63.5	12.6	159	6	5208144-35	Patent No. 5208144
C 36	63.5	12.6	182	2	US-09-940-236-3495	Sequence 3495, Ap
C 37	63.5	12.6	208	2	US-09-252-991A-29277	Sequence 29277, A
C 38	63.5	12.6	640	2	US-09-177-165A-30	Sequence 30, Appl
C 39	63	12.5	442	2	US-09-902-540-11579	Sequence 11579, A
C 40	63	12.5	490	2	US-09-270-767-44437	Sequence 44437, A
C 41	62.5	12.5	138	2	US-09-270-767-37396	Sequence 37396, A
C 42	62.5	12.5	138	2	US-09-270-767-52613	Sequence 52613, A
C 43	62.5	12.5	188	2	US-09-252-991A-32431	Sequence 32431, A
C 44	62.5	12.5	536	2	US-09-949-016-10134	Sequence 10134, A
C 45	62.5	12.5	602	2	US-09-252-991A-17752	Sequence 17752, A

ALIGNMENTS

RESULT 1

US-09-949-016-10507
; Sequence 10507, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10507
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10507

Alignment Scores:
Pred. No.: 0.000163 Length: 187
Score: 97.50 Matches: 23
Percent Similarity: 46.2% Conservative: 13
Best Local Similarity: 29.5% Mismatches: 35
Query Match: 19.4% Indels: 7
DB: 2 Gaps: 2

US-10-079-954-2 (1-261) x US-09-949-016-10507 (1-187)

Qy 37 TGTCATGCTTGTGAGAGAGAAAACCTTTCGATGCGAGAACCCAGGAGGTGCATATGG 96

Db 60 CysHisAspCysAlaValIleAsnAspPheAsnCysProAlaIleArgValCysProTyr 79
Qy 97 ACAGAGCCATCTACTGGTTATAGCGCGCGTGAATAATTTCCACGTTTTCATGGTTGCG 156
Db 80 HisIleArgAgCysMetThrIleSerIleArgIleAsnSerArgGluLeuValTyr 99
Qy 157 AACAGGTCTCGCTGGTTGT-----GCAGGATGGAGAGACCCAGCCAGAG 204
Db 100 LysAsnCysThrAsnAsnCysThrPheValTyrAlaAlaGluInProProGluAlaPro 119
Qy 205 GAGAGCGGTTCTCCTCGAAGACCCATCGCTTCTTTACCTCAAGTGTGT 258
Db 120 GlyLysIlePhe-----LysThrAsnSerPheTyrIrpValCysCys 134

RESULT 2

US-09-252-991A-28542
; Sequence 28542, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28542
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-28542
Alignment Scores:
Pred. No.: 0.195 Length: 159
Score: 75.00 Matches: 17
Percent Similarity: 41.8% Conservative: 6
Best Local Similarity: 30.9% Mismatches: 20
Query Match: 14.9% Indels: 12
DB: 2 Gaps: 2

US-10-079-954-2 (1-261) x US-09-252-991A-28542 (1-159)

Qy 46 TGTGAGAGAGAAACACTTTCGAGTGCAGAACCCAGGAGGTGCAATGG----- 96
Db 106 CysThrArgSerSerArgGlyTyrCysValThrProArgAlaCysArgTyrArgThr 125
Qy 97 ACAGAGCCATCTACTGGTTATAGCGCGCGTGAATAATTTCCACGTTTTCATGGTTGCG 156
Db 126 SerThrSerArgCysSerProAlaAla-----SerThr 136
Qy 157 AACAGGTCTCGCTGGTTGTTCGACGATGGAGAGACCCAGCCAGCCA 201
Db 137 SerThrCysArgProGlyCysThrSerMetThrArgProArgPro 151

RESULT 3

US-09-252-991A-20192
; Sequence 20192, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20192
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20192

Alignment Scores:
Pred. No.: 0.345 Length: 136
Score: 73.00 Matches: 17
Percent Similarity: 49.0% Conservative: 7
Best Local Similarity: 34.7% Mismatches: 17
Query Match: 14.5% Indels: 8
DB: 2 Gaps: 2

US-10-079-954-2 (1-261) x US-09-252-991A-20192 (1-136)

Qy 70 TGCAGAACCCAGGAGGTGCAATGCACAGACCATCTCGTTATAGCGCGGTGAAA 129
Db 29 CysSerAsnGlyTyrArgCysArgSerAlaArgPro-----Thr 41
Qy 130 ATATTTCCACGTTTTTTCATGGTTCACACAGGTGCTCCGCTGCT---TGTGAGCCATG 186
Db 42 ValSerGlyArgAlaAlaAlaIleArgArgCysSerAlaGlyArgCysAlaSerAla 61
Qy 187 GAGAGACCCAGCCAGGAGGAGACCGG 213
Db 62 AspAlaProArgProTyrArgArgArg 70

RESULT 4

US-09-248-796A-17746
; Sequence 17746, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17746
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Candida albicans

US-09-248-796A-17746

Alignment Scores:
Pred. No.: 0.821 Length: 350
Score: 71.50 Matches: 26
Percent Similarity: 53.4% Conservative: 21
Best Local Similarity: 29.5% Mismatches: 19
Query Match: 14.2% Indels: 22
DB: 2 Gaps: 6

US-10-079-954-2 (1-261) x US-09-248-796A-17746 (1-350)

Qy 234 CATGGGCTCTCCAGGAGAACCGCTCTCC-----TCTGG 199
Db 247 HisGlyLeuAlaLysGlu-AsnSerPheSerLeuAsnPheIleSerSerIleMetAlaG 266
Qy 198 CTGGGGTCTCTCCATCGCTGCACAAACCCAGCGAGACCTGTTG---CGAACCATGAAAA 142
Db 266 YLeuGlyValAlaIleValMetAsnProTyrAspValIleValThrArgMetTyrAsnG 286
Qy 141 ACGTGGAATATTTTACGCGCGGTATACGCGGTATACGCGGTAT-----GG 103
Db 286 nLysGlyAsnLeuTyr-SerGlyProIleAspCysPheLysThrIleAlaGluG 306

QY 102 CTCTGTCCATTTCACCTCCTTGGGTTCTGGCACTCGAAAGTGTTTTCTCTCACAAAGC 43
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 306 yAlaMetaLaLeuTyR---LysGlyPheTrp---AlaGlnLeuPheArgIleGlyPro-- 323
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
QY 42 ATGACACCACACTCTATTGTCA 21
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 324 -----HisThrIleLeuThr 328
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
RESULT 5
US-09-740-041-2
; Sequence 2, Application US/09740041
; Patent No. 6562593
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001001
; CURRENT APPLICATION NUMBER: US/09/740,041
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Human
US-09-740-041-2

Alignment Scores:
Pred. No.: 1.02 Length: 589
Score: 71.50 Matches: 27
Percent Similarity: 35.1% Conservative: 13
Best Local Similarity: 23.7% Mismatches: 33
Query Match: 14.2% Indels: 41
DB: 2 Gaps: 5

US-10-079-954-2 (1-261) x US-09-740-041-2 (1-589)
QY 234 CATGGCTCTCCAGGAGAACCGCTCTCTCTGGCTGGTGGTCTCTCCATGGCTGCACA 175
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 254 TyrGlyMetPheGlyIleTrpTyrMetPheTrpLeuGlnAlaTyrGluCysPro 273
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
QY 174 ACCAGCGAGCCTGTTCGCAACCATGAATAAAGCTGG-----AAATATTTTCAC 124
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 274 AlaAlaHisProThrIleSerAsnGluGlySerThrIleGluThrSerIleGlyGlu 293
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
QY 123 GCGCGTATAACGAGTAGTGTCTGTCCATTGCCACCTCTCTGG----- 79
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 294 GlyAla---AsnValValSerLeuSerLysPheSerThrProTyrLysArgPheThr 312
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
QY 78 -----GTTCTCGCACTC----- 67
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 313 SerLeuProValTyrAlaIleIleValAlaAlaenPheCysArgSerTrpThrPheTyrLeu 332
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
QY 66 -----GAAAGTGTTTTTC----- 55
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 333 LeuLeuIleSerGlnProAlaTyrPheGluGluValPheGlyPheAlaIleSerLysVal 352
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
QY 54 TCTCTCACAGATGACACGACACTCTATTGTCCCTCGTC 13
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 353 GlyLeuLeuSerAlaValProHisMetValMetThrIleVal 366
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
RESULT 6
US-09-252-991A-18870
; Sequence 18870, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubinfeld et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A

US-10-079-954-2 (1-261) x US-09-252-991A-18870 (1-441)
QY 234 CATGGCTCTTCCAGGAGAACCGCTCTCTCTGGCTGGTGGTCTCTCCATGGCTGC 178
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 385 HisSerCysProGlnAlaArgProArgLeuGlnProTrpLeuThrSer-----Cys 401
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
QY 177 ACAACGAGCGGAGCACCTGTTCGCAACCATGAATAAAGCTGGAAATATTTTCACGGCCGC 118
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 402 SerThrProSerSerProAlaSer-----ProTrpProTrp----- 413
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
QY 117 TATAACGAGTAGTGTCTCTCTGGCTGGTGGTCTCTCCATGGCTGGTGGTGGTGGTGGT 58
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 414 -----TrpLeuAlaProTrpAlaProSerTrpSerGlyGlyTyrProIle 429
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
QY 57 TTCTCTCTCACAGCATGACACACAC 31
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
Db 430 SerAlaIleProCysProThrProHis 438
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
RESULT 7
US-09-364-206-47
; Sequence 47, Application US/09364206
; Patent No. 6475752
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Baugh, Mariah R.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: Mammalian Imidazoline Receptor
; FILE REFERENCE: PC-0006 US
; CURRENT APPLICATION NUMBER: US/09/364,206
; CURRENT FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PERL Program
; SEQ ID NO 47
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY:
; OTHER INFORMATION: W43396
; PUBLICATION INFORMATION:
US-09-364-206-47

Alignment Scores:
Pred. No.: 2.58 Length: 559
Score: 68.50 Matches: 22
Percent Similarity: 33.7% Conservative: 7
Best Local Similarity: 25.6% Mismatches: 27
Query Match: 13.6% Indels: 30
DB: 2 Gaps: 2

US-10-079-954-2 (1-261) x US-09-364-206-47 (1-559)

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QY 214 ACCGTTCTCTGGCTGGCTCTCTCCATCGTGCACACCGAGCGACCTGTTC 155
Db 377 ThrArgSerLeuSerTrpThrProProThr-CysThrSerSer----- 391
QY 154 GAACCATGAAAAACGTGGAATATTTTTCAGCGCGCTATACGACGATGCTCTGTCC 95
Db 392 -----ThrTrpThrCysAlaHisAlaLeuHisProSerThrTrpProCysCy 407
QY 94 ATTGCACTCTCT----- 82
Db 407 sValAlaProSerSerThrAlaAlaThrProAlaCysArgSerSerCysAlaSerCysSe 427
QY 81 -----TGGGTCTGGCACTCGAAGTGTCTCTCTCACAAGCATGACACC 35
Db 427 rProSerThrArgTrpLeuAlaAlaAlaArgSerAlaAlaAlaAlaAlaSerProSerTh 447

QY 34 ACACCTCTATTGTCC 19
Db 447 rTrpSerThrValThr 452

RESULT 8
US-09-817-514A-4
; Sequence 4, Application US/09817514A
; Patent No. 6639129
; GENERAL INFORMATION:
; APPLICANT: ffrench-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rocheleau, Thomas
; APPLICANT: Waterfield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/09/817,514A
; PRIORITY FILING DATE: 2000-03-26
; PRIOR FILING DATE: US 60/191806
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1476
; TYPE: PRT
; ORGANISM: Photorhabdus luminescens
US-09-817-514A-4

Alignment Scores:
Pred. No.: 4.51 Length: 1476
Score: 68.00 Matches: 23
Percent Similarity: 42.9% Conservative: 7
Best Local Similarity: 32.9% Mismatches: 22
Query Match: 13.5% Indels: 18
DB: 2 Gaps: 3

US-10-079-954-2 (1-261) x US-09-817-514A-4 (1-1476)
QY 53 GAGAAACACTTTCAGTGCACAGCCAGAGGTGCAATGGACAGACCATCTGCG 112
Db 791 GluGlnThrAspSerHisGlnLeuAlaGlnGlyAsnAlaProGluArgThrProProAla 810
QY 113 TTATAGCGCGCGTGAATAATATTCACGTTTTTTCATGGTTTCGCAACAGGTGCTCCGCTG 172
Db 811 LeuThrLys-----SerTrpTrpAlaThrGlyLeuProAla 822
QY 173 GTT-----GTGCAGCGATGGAGAGACCCAGCCAGAGGAGAGCGGTTC 217
Db 823 ValAspAsnAlaLeuSerAlaGlyTyrTrpArgGlyAspLysGlnAlaPheAlaGlyPhe 842
QY 218 TCCTGGAAGAGCCCATGCTCTCTTTTACC 247
Db 843 Thr-----ProArgPheThr 847

RESULT 9
US-09-270-767-45485
; Sequence 45485, Application US/09270767
; Patent No. 6703491

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; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45485
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45485

Alignment Scores:
Pred. No.: 2.48 Length: 234
Score: 67.50 Matches: 26
Percent Similarity: 38.5% Conservative: 9
Best Local Similarity: 28.6% Mismatches: 31
Query Match: 13.4% Indels: 25
DB: 2 Gaps: 4

US-10-079-954-2 (1-261) x US-09-270-767-45485 (1-234)
QY 198 CTTGGGTCTCTCCATCGTGC-----ACACGAGCGGACCATCTGTTCG----- 154
Db 133 LeuAsnProLeuHisArgCysGluLeuArgSerThrGluThrProLeuAlaAlaLeuSer 152
QY 153 -----AACCATGAAAAACGTGGAATATTTTTCACGGCGCGCTAT 115
Db 153 PheAlaHisThrTyrThrArgThrHisArgLysLysValleTyrTyrLeuCysGlyLeuPhe 172
QY 114 AACGAGTATGCTCTGTCATTTGCACCTCTCTGGGTTCTGCACCTCGAA----- 64
Db 173 TyrLeuThrHisAlaCysValPheAlaProTyrPheIlePheAlaLeuArgIlePheVal 192
QY 63 -----AGTGTTCCTCTCAGCAGCATGACACCATCTATT--- 25
Db 193 ProLeuValGlyLeuPheSerValLeuLeuValAlaGlnThrSerAspAsnIleGlu 212
QY 24 -----GTCACTCTGCTCGTTCGCTGGCT 1
Db 213 CysIleAlaValThrAlaSerArgCysIleAla 223

RESULT 10
US-09-540-236-3415
; Sequence 3415, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3415
; LENGTH: 598
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3415

Alignment Scores:
Pred. No.: 4.28 Length: 598
Score: 67.00 Matches: 18
Percent Similarity: 51.5% Conservative: 16
Best Local Similarity: 27.3% Mismatches: 27
Query Match: 13.3% Indels: 5
DB: 2 Gaps: 2

US-10-079-954-2 (1-261) x US-09-540-236-3415 (1-598)

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RESULT 12
US-09-852-100B-4
; Sequence 4, Application US/09852100B
; Patent No. 6787319

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; SEQ ID NO 142
; LENGTH: 312
; TYPE: PRT
; ORGANISM: mouse

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US-09-188-930-142

Alignment Scores:

Pred. No.: 4.5 Length: 312
Score: 66.00 Matches: 17
Percent Similarity: 51.7% Conservative: 14
Best Local Similarity: 28.3% Mismatches: 19
Query Match: 13.1% Indels: 10
DB: 2 Gaps: 3

US-10-079-954-2 (1-261) x US-09-188-930-142 (1-312)

Qy 197 TTGGTCTCTCCATCGTCACACACGCGAGCAGCTGTTCGACCATGAAAAACGT 138
Db 110 LeuGlyValLysIleSerGluGlnGlnAlaGluLysIleLeuLysSerMetAspLysAsn 129
Qy 137 GGAATATTTTCACGCGCGCTATACGAGTATGGCTCTGTCCATTG----- 90
Db 130 GlyThrMet---ThrIleAspTrpAsnGluTrpArgAspTyrHisLeuLeuHisProVal 148
Qy 89 -----CACCTCTGGTCTGG---CACTCGAAGTGTTCCTCTCTCACAA 45
Db 149 GluAsnIleProGluIleLeuTyrTrpLysHisSerThrIlePheAspValGlyGlu 168

RESULT 14

US-09-312-283C-142

; Sequence 142, Application US/09312283C

; Patent No. 6573095

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Onrust, Rene

; APPLICANT: Murison, James G.

; APPLICANT: Kumble, Krishanand D.

; TITLE OF INVENTION: Compositions Isolated from Skin Cells

; FILE REFERENCE: 11000.1011C2

; CURRENT APPLICATION NUMBER: US/09/312,283C

; NUMBER OF SEQ ID NOS: 425

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 142

; LENGTH: 312

; TYPE: PRT

; ORGANISM: Mouse

US-09-312-283C-142

Alignment Scores:

Pred. No.: 4.5 Length: 312
Score: 66.00 Matches: 17
Percent Similarity: 51.7% Conservative: 14
Best Local Similarity: 28.3% Mismatches: 19
Query Match: 13.1% Indels: 10
DB: 2 Gaps: 3

US-10-079-954-2 (1-261) x US-09-312-283C-142 (1-312)

Qy 197 TTGGTCTCTCCATCGTCACACACGCGAGCAGCTGTTCGACCATGAAAAACGT 138
Db 110 LeuGlyValLysIleSerGluGlnGlnAlaGluLysIleLeuLysSerMetAspLysAsn 129
Qy 137 GGAATATTTTCACGCGCGCTATACGAGTATGGCTCTGTCCATTG----- 90
Db 130 GlyThrMet---ThrIleAspTrpAsnGluTrpArgAspTyrHisLeuLeuHisProVal 148
Qy 89 -----CACCTCTGGTCTGG---CACTCGAAGTGTTCCTCTCTCACAA 45
Db 149 GluAsnIleProGluIleLeuTyrTrpLysHisSerThrIlePheAspValGlyGlu 168

RESULT 15

US-09-561-077C-64

; Sequence 64, Application US/09561077C

; Patent No. 6706501
; GENERAL INFORMATION:
; APPLICANT: Robson, Reinhardt D.
; APPLICANT: Deng, Ming-de
; APPLICANT: Grund, Alan D.
; TITLE OF INVENTION: LINOLEATE ISOMERASE
; FILE REFERENCE: 3161-20-C1
; CURRENT APPLICATION NUMBER: US/09/561,077C
; CURRENT FILING DATE: 2000-04-28
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Propionibacterium acnes
US-09-561-077C-64

Alignment Scores:

Pred. No.: 4.76 Length: 358
Score: 66.00 Matches: 26
Percent Similarity: 45.9% Conservative: 8
Best Local Similarity: 35.1% Mismatches: 21
Query Match: 13.1% Indels: 19
DB: 2 Gaps: 4

US-10-079-954-2 (1-261) x US-09-561-077C-64 (1-358)

Qy 198 CTTGGTCTCTCCATCGTCACACACGCGAGCAGCTGTTCGACCATGAAAAA--- 142
Db 286 ValGlyThrValGluSerValThrThrLeuSerAla-----GlyAsnAlaAlaLysMet 303
Qy 141 -----ACGTGGAATATTTTCACGGCGCTATACGCAGTA----- 106
Db 304 TyrIleGlyThrProLysGlnPheProAspArgTyrArgAlaValAsnSerSerThr 323
Qy 105 TGGCTCTGTCATTTGCACCTCTTGGTGTTCGCACTCGAAGTGTTCCTCTCTCACA 46
Db 324 TrpIleThrProGlnAlaProProThrMetVal-----Ile-Gl 336
Qy 45 AGCATGACACACACACTCTATTGTCACTCGCTCGGTTCCG 6
Db 336 nGlyAsnHisAspThrPheValProProSerSerValArg 349

Search completed: March 23, 2006, 12:49:03

Job time : 25.8548 secs

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:49:19 ; Search time 2.44839 Seconds
(without alignments)
694.416 Million cell updates/sec

Title: US-10-079-954-1
Perfect score: 564
Sequence: 1 gcaatgatgggcatcctt.....ccatcaagaagattatggtt 297

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 159630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 339260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/abs/ASSWEB_spool/US1007954/runat_23032006_102937_1988/app_query.fasta_1
-DB=Published Applications AA New -QFMT=fastan -SUFFIX=rapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DICALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs02p
-USER=US1007954@cgn1_1_24 @runat_23032006_102937_1988 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA New:
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US16_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	453	80.3	241	7	US-11-019-711-77 Sequence 77, Appl
2	453	80.3	241	7	US-11-019-711-78 Sequence 78, Appl
3	453	80.3	241	7	US-11-234-786-114 Sequence 114, Appl
4	371	65.8	240	7	US-11-019-711-76 Sequence 76, Appl
5	358	63.5	126	5	US-09-978-360A-555 Sequence 555, Appl
6	357.5	63.4	241	7	US-11-019-711-22 Sequence 22, Appl
7	172.5	30.6	222	7	US-11-019-711-81 Sequence 81, Appl
8	158	28.0	247	7	US-11-019-711-79 Sequence 79, Appl
9	137.5	24.4	237	7	US-11-108-172-1062 Sequence 1062, Appl

10	137.5	24.4	243	7	US-11-108-172-1122 Sequence 1122, Ap
11	137.5	24.4	344	7	US-11-108-172-1085 Sequence 1085, Ap
12	137.5	24.4	446	7	US-11-108-172-1121 Sequence 1121, Ap
13	131	23.2	253	6	US-10-501-035-248 Sequence 248, Appl
14	130	23.0	227	7	US-11-029-188-6 Sequence 6, Appl
15	130	23.0	228	6	US-10-821-234-1266 Sequence 1266, Ap
16	130	23.0	282	7	US-11-019-711-80 Sequence 80, Appl
17	129.5	23.0	267	6	US-10-627-952-20 Sequence 20, Appl
18	129.5	23.0	267	6	US-10-329-258-25 Sequence 25, Appl
19	129.5	23.0	327	6	US-10-821-234-1686 Sequence 1686, Ap
20	112.5	19.9	270	6	US-10-453-372-462 Sequence 462, App
21	112.5	19.9	270	6	US-10-453-372-464 Sequence 464, App
22	104	18.4	80	6	US-10-475-075-860 Sequence 860, App
23	84.5	15.0	172	6	US-10-517-696-108 Sequence 108, App
24	82.5	14.6	204	7	US-11-080-991-8 Sequence 8, Appl
25	78	13.8	204	7	US-11-096-568A-23452 Sequence 23452, A
26	78	13.8	220	7	US-11-096-568A-23451 Sequence 23451, A
27	78	13.8	282	7	US-11-096-568A-23450 Sequence 23450, A
28	77	13.7	5405	7	US-11-108-172-1116 Sequence 1116, Ap
29	76	13.5	533	7	US-11-214-199-63 Sequence 63, Appl
C 30	75.5	13.4	343	7	US-11-096-568A-23765 Sequence 23765, A
C 31	75	13.3	706	7	US-11-072-512-2456 Sequence 2456, Ap
32	74	13.1	123	7	US-11-096-568A-25201 Sequence 25201, A
33	74	13.1	222	7	US-11-096-568A-19585 Sequence 19585, A
C 34	74	13.1	245	7	US-11-096-568A-16703 Sequence 16703, A
C 35	74	13.1	273	7	US-11-096-568A-16702 Sequence 16702, A
C 36	74	13.1	340	7	US-11-096-568A-16701 Sequence 16701, A
37	73.5	13.0	168	7	US-11-044-111-27 Sequence 27, Appl
38	73	12.9	194	7	US-11-087-099-10091 Sequence 10091, A
39	72	12.8	428	7	US-11-096-568A-19503 Sequence 19503, A
40	72	12.8	468	7	US-11-087-099-10159 Sequence 10159, A
41	72	12.8	544	7	US-11-096-568A-19501 Sequence 19501, A
C 42	71.5	12.7	3375	7	US-11-044-111-23 Sequence 23, Appl
43	71	12.6	199	7	US-11-179-018-2 Sequence 2, Appl
44	71	12.6	244	7	US-11-087-099-9456 Sequence 9456, Ap
45	71	12.6	339	7	US-11-174-816-55 Sequence 55, Appl

ALIGNMENTS

RESULT 1
US-11-019-711-77
; Sequence 77, Application US/11019711
; Publication No. US20060009634A1
; GENERAL INFORMATION:
; APPLICANT: Kikuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Bainger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigara, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eissen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235

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; CURRENT APPLICATION NUMBER: US/11/019,711
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/037,417
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-019-711-77

Alignment Scores:
Pred. No.: 1 38e-39 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 7 Gaps: 0

US-10-079-954-1 (1-297) x US-11-019-711-77 (1-241)
QY 1 GCAATCGATGGGCACTCTTTCTGAAGATCTTCGGGCCACTGTGTCGATGCCATGCAG 60
Db 33 SerIleAspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerAlaMetGln 52
QY 61 TTTGTCAACGTGGGCTACTTCTCATCCACCGCGGTGTGGCTTCTTGGTTTC 120
Db 53 PheValAsnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72
QY 121 CTGGCTGCTATGGTCTAGACTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATC 180
Db 73 LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe 92
QY 181 CTCCTCCTCATCTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 240
Db 93 LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaLeuValTyrThrThr 112
QY 241 ATGGCTGAGCACTTCCCGACGTTGCTGTAGTCTGCTGCTGCTGCTGCTGCTGCT 288
Db 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

RESULT 2
US-11-019-711-78
; Sequence 78, Application US/11019711
; Publication No. US20060009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsbrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
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; PRIOR APPLICATION NUMBER: US/10/037,417
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/260,018
 ; PRIOR FILING DATE: 2001-01-05
 ; PRIOR APPLICATION NUMBER: 60/260,360
 ; PRIOR FILING DATE: 2001-01-08
 ; PRIOR APPLICATION NUMBER: 60/272,411
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: 60/272,817
 ; PRIOR FILING DATE: 2001-03-02
 ; PRIOR APPLICATION NUMBER: 60/291,186
 ; PRIOR FILING DATE: 2001-05-15
 ; PRIOR APPLICATION NUMBER: 60/303,231
 ; PRIOR FILING DATE: 2001-07-05
 ; PRIOR APPLICATION NUMBER: 60/305,060
 ; PRIOR FILING DATE: 2001-07-12
 ; PRIOR APPLICATION NUMBER: 60/318,405
 ; PRIOR FILING DATE: 2001-09-10
 ; PRIOR APPLICATION NUMBER: 60/318,700
 ; PRIOR FILING DATE: 2001-09-12
 ; NUMBER OF SEQ ID NOS: 227
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 22
 ; LENGTH: 241
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-019-711-22

Alignment Scores:
 Pred. No.: 1,21e-29 Length: 241
 Score: 357.50 Matches: 73
 Percent Similarity: 85.4% Conservative: 9
 Best Local Similarity: 76.0% Mismatches: 13
 Query Match: 63.4% Indels: 1
 DB: 7 Gaps: 1

US-10-079-954-1 (1-297) x US-11-019-711-22 (1-241)

Qy 4 ATCGATGGGCATCTTCTGAAGATCTTCGGGCACCTGCTCCAGTCCAGTCCAGTTT 63
 Db 34 ValaspGlyThrSerPheLeuValPheGlySerLeuSerSerSerAlaMetGlnPhe 53
 Qy 64 GTCAACGTGGCTACTTCTCATCCAGCCGCGTGTGTCTTGTCTTGTCTTGTCTTGTCTG 123
 Db 54 ValaenValGlyTyrrPheLeuLeuAlaGlyAlaValLeuPheLeuPheGlyPheLeu 73
 Qy 124 GGCTGCTATGCTGCTAAGACTGAGACGACGACGACGACGACGACGACGACGACGACGAC 180
 Db 74 GlyCysTyrrGlyAlaProSerGluLeuValValCysAlaLeuValMetPhePheSerIle 93
 Qy 181 CTCCTCTCATCTTCTATTCATTCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Db 94 LeuLeuLeuLeuPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 113
 Qy 241 ATGCTGAGCACTTCCCGACGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 288
 Db 114 LeuAlaGluGlnPheLeuThrLeuLeuValValProAlaIleGluLys 129

RESULT 7

US-11-019-711-81
 ; Sequence 81, Application US/11019711
 ; Publication No. US20060009634A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Alsbrook II, John P
 ; APPLICANT: Tchernev, Velizar T
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Spytek, Kimberly A
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Grosse, William M
 ; APPLICANT: Lepley, Denise M
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Vernet, Corine A.M.

; APPLICANT: Li, Li
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Edinger, Shlomit R
 ; APPLICANT: Sciore, Paul
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Malyankar, Uriel M
 ; APPLICANT: Rothenberg, Mark
 ; APPLICANT: Stone, David J
 ; APPLICANT: Boldog, Ferenc L
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Shenoy, Suresh G
 ; APPLICANT: Anderson, David W
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Taupier Jr, Raymond J
 ; APPLICANT: Miller, Charles E
 ; APPLICANT: Eisen, Andrew J
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-235
 ; CURRENT APPLICATION NUMBER: US/11/019,711
 ; CURRENT FILING DATE: 2004-12-21
 ; PRIOR APPLICATION NUMBER: US/10/037,417
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: 60/260,018
 ; PRIOR FILING DATE: 2001-01-05
 ; PRIOR APPLICATION NUMBER: 60/260,360
 ; PRIOR FILING DATE: 2001-01-08
 ; PRIOR APPLICATION NUMBER: 60/272,411
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: 60/272,817
 ; PRIOR FILING DATE: 2001-03-02
 ; PRIOR APPLICATION NUMBER: 60/291,186
 ; PRIOR FILING DATE: 2001-05-15
 ; PRIOR APPLICATION NUMBER: 60/303,231
 ; PRIOR FILING DATE: 2001-07-05
 ; PRIOR APPLICATION NUMBER: 60/305,060
 ; PRIOR FILING DATE: 2001-07-12
 ; PRIOR APPLICATION NUMBER: 60/318,405
 ; PRIOR FILING DATE: 2001-09-10
 ; PRIOR APPLICATION NUMBER: 60/318,700
 ; PRIOR FILING DATE: 2001-09-12
 ; NUMBER OF SEQ ID NOS: 227
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 81
 ; LENGTH: 222
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Tetraspanin
 ; OTHER INFORMATION: Family Consensus Sequence
 US-11-019-711-81

Alignment Scores:
 Pred. No.: 2,21e-10 Length: 222
 Score: 172.50 Matches: 37
 Percent Similarity: 64.9% Conservative: 13
 Best Local Similarity: 48.1% Mismatches: 22
 Query Match: 30.6% Indels: 5
 DB: 7 Gaps: 1

US-10-079-954-1 (1-297) x US-11-019-711-81 (1-222)

Qy 4 ATCGATGGGCATCTTCTGAAGATCTTCGGGCACCTGCTCCAGTCCAGTCCAGTTT 63
 Db 27 ValaspLeuSerSerPheSerGluLeuLeuGlySerLeuSerSer----- 41
 Qy 64 GTCAACGTGGCTACTTCTCATCGACGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 123
 Db 42 LeuValAlaAlaTyrrValLeuLeuAlaValGlyAlaIleLeuPheLeuValGlyPheLeu 61
 Qy 124 GGCTGCTATGCTGCTAAGACTGAGACGACGACGACGACGACGACGACGACGACGACGAC 183
 Db 62 GlyCysCysGlyAlaIleArgGluSerArgCysLeuLeuGlyLeuTyrrPheValPheLeu 81


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; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1121
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-172-1121

Alignment Scores:
Pred. No.: 1e-06 Length: 446
Score: 137.50 Matches: 30
Percent Similarity: 59.4% Conservative: 11
Best Local Similarity: 43.5% Mismatches: 27
Query Match: 24.4% Indels: 1
DB: 7 Gaps: 1

US-10-079-954-1 (1-297) x US-11-108-172-1121 (1-446)
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; Sequence 248, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR P
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROS
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 248
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-248

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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(without alignments)
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Title: US-10-079-954-1

Perfect score: 564

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	453	80.3	233	3	US-09-148-545-137
3	453	80.3	233	5	US-10-979-111-137
4	453	80.3	241	3	US-09-759-143-114
5	453	80.3	241	3	US-09-780-669-114
6	453	80.3	241	3	US-09-030-606-114
7	453	80.3	241	3	US-09-822-827-114
8	453	80.3	241	3	US-09-115-453-114
9	453	80.3	241	3	US-09-232-880-114
10	453	80.3	241	3	US-09-908-193-44
11	453	80.3	241	3	US-09-895-793-114
					Sequence 137, App
					Sequence 137, App
					Sequence 137, App
					Sequence 114, App
					Sequence 114, App
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					Sequence 114, App
					Sequence 114, App
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					Sequence 114, App

Sequence 114, App
Sequence 114, App
Sequence 326, App
Sequence 114, App
Sequence 425, App
Sequence 114, App
Sequence 604, App
Sequence 114, App
Sequence 77, Appl
Sequence 78, Appl
Sequence 114, App
Sequence 425, App
Sequence 326, App
Sequence 424, App
Sequence 423, App
Sequence 423, App
Sequence 324, App
Sequence 20, Appl
Sequence 1489, Ap
Sequence 4346, Ap
Sequence 43, Appl
Sequence 76, Appl
Sequence 3062, Ap
Sequence 555, App
Sequence 22, Appl
Sequence 6493, Ap
Sequence 19, Appl
Sequence 81, Appl
Sequence 39, Appl
Sequence 76, Appl
Sequence 42, Appl
Sequence 72, Appl

ALIGNMENTS

RESULT 1

US-09-981-876-137
; Sequence 137, Application US/09981876
; Patent No. US20020164669A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,161
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; PRIOR APPLICATION NUMBER: 60/040,626
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; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502

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3	PRIOR APPLICATION NUMBER:	60/056,662
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8	PRIOR FILING DATE:	1997-08-22
9	PRIOR APPLICATION NUMBER:	60/056,637
10	PRIOR FILING DATE:	1997-08-22
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22	PRIOR FILING DATE:	1997-08-22
23	PRIOR APPLICATION NUMBER:	60/056,636
24	PRIOR FILING DATE:	1997-08-22
25	PRIOR APPLICATION NUMBER:	60/056,874
26	PRIOR FILING DATE:	1997-08-22
27	PRIOR APPLICATION NUMBER:	60/056,910
28	PRIOR FILING DATE:	1997-08-22
29	PRIOR APPLICATION NUMBER:	60/056,864
30	PRIOR FILING DATE:	1997-08-22
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33	PRIOR APPLICATION NUMBER:	60/056,845
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37	PRIOR APPLICATION NUMBER:	60/047,595
38	PRIOR FILING DATE:	1997-05-23
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55	PRIOR APPLICATION NUMBER:	60/043,578
56	PRIOR FILING DATE:	1997-04-11
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59	PRIOR APPLICATION NUMBER:	60/047,501
60	PRIOR FILING DATE:	1997-05-23
61	PRIOR APPLICATION NUMBER:	60/043,670
62	PRIOR FILING DATE:	1997-04-11
63	PRIOR APPLICATION NUMBER:	60/056,632
64	PRIOR FILING DATE:	1997-08-22
65	PRIOR APPLICATION NUMBER:	60/056,664
66	PRIOR FILING DATE:	1997-08-22
67	PRIOR APPLICATION NUMBER:	60/056,876
68	PRIOR FILING DATE:	1997-08-22
69	PRIOR APPLICATION NUMBER:	60/056,881

; PRIOR FILING DATE: 1997-08-22
 ; PRIOR APPLICATION NUMBER: 60/056,909
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 ; PRIOR APPLICATION NUMBER: 60/056,887
 ; PRIOR FILING DATE: 1997-08-22
 ; PRIOR APPLICATION NUMBER: 60/056,908
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 ; PRIOR APPLICATION NUMBER: 60/048,964
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/057,650
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/056,884
 ; PRIOR FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 280
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 137
 ; LENGTH: 233

Alignment Scores:
 Pred. No.: 3.33e-40 Length: 233
 Score: 453.00 Matches: 93
 Percent Similarity: 97.9% Conservative: 1
 Best Local Similarity: 96.9% Mismatches: 2
 Query Match: 80.3% Indels: 0
 DB: 3 Gaps: 0

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Qy	181	CTCTCTCTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	240
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 ; Publication No. US20030027132A1
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 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 70 Human Secreted Proteins
 ; FILE REFERENCE: P2001P1
 ; CURRENT APPLICATION NUMBER: US/09/148,545
 ; CURRENT FILING DATE: 1998-09-04
 ; EARLIER APPLICATION NUMBER: PCT/US98/04482
 ; EARLIER FILING DATE: 1998-03-06
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; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 233

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Pred. No.: 3,33e-40 Length: 233
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: Gaps: 0

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Qy 121 CTGGGCTGCTATGGTGTCAAGACTGAGAGCAAGTGTGCCCTCGTGAGTCTTCTTCATC 180
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; Sequence 137, Application US/10979111
; Publication No. US20050215775A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins

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CURRENT APPLICATION NUMBER: US/10/979,111
CURRENT FILING DATE: 2004-11-02
PRIOR APPLICATION NUMBER: US/09/621,011
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: 09/148,545
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,333
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/038,621
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,161
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,626
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,334
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,336
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,163
PRIOR FILING DATE: 1997-03-07
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SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 137
LENGTH: 233
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (233)
OTHER INFORMATION: Xaa equals stop translation
US-10-979-111-137

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Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
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Query Match: 80.3% Indels: 0
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Sequence 114, Application US/09759143
Patent No. US200202248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.

FILE REFERENCE: PZ001P1
CURRENT APPLICATION NUMBER: US/10/979,111
CURRENT FILING DATE: 2004-11-02
PRIOR APPLICATION NUMBER: US/09/621,011
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: 09/148,545
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,333
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PRIOR APPLICATION NUMBER: 60/040,163
PRIOR FILING DATE: 1997-03-07
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 280
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SEQ ID NO 137
LENGTH: 233
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (233)
OTHER INFORMATION: Xaa equals stop translation
US-10-979-111-137

Alignment Scores:
Pred. No.: 3,33e-40 Length: 233
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.3% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 5 Gaps: 0

US-10-079-954-1 (1-297) x US-09-759-143-114 (1-241)

Qy 1 GCAATCGATGGGCGATCTTTCTGAAGATCTTCGGGCGACTGTCGTCAGTGCATGCAG 60
Db 33 SerileaspGlyAlaSerPheLeuLysilePheGlyProLeuSerSerAlaMetGln 52
Qy 61 TTTGTCAACGTGGGCTACTTCTCATCGACCGCGGCTTGTGGTCTTTGCTCTTGGTTTC 120
Db 53 PheValasnValGlyTyPheLeuLysileAlaGlyValValPheAlaLeuGlyPhe 72
Qy 121 CTGGGCTGCTATGGTGTCTAAGACTGAGCAAGTGTGCCCTGTCGACGTTCTTCTTCATC 180
Db 73 LeuGlyCysTyrglyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePheile 92
Qy 181 CTCTCTCATCTTCTTCATTCGTCAGGTTGCAGCTGTCAGCTGTCGCTGGTGTGATCACCATA 240
Db 93 LeuLeuLeuilePheileAlaGluValAlaAlaValValAlaLeuValTyThr 112
Qy 241 ATGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCTGCATCAAGAAG 288
Db 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaileLysLys 128

RESULT 5
US-09-780-669-114
Sequence 114, Application US/09780669
Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, William
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 114
LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapien
US-09-759-143-114

Alignment Scores:
Pred. No.: 3,35e-40 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 3 Gaps: 0
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Pred. No.:	3.35e-40	Length:	241
Score:	453.00	Matches:	93
Percent Similarity:	97.9%	Conservative:	1
Best Local Similarity:	96.9%	Mismatches:	2
Query Match:	80.3%	Indels:	0
DB:	3	Gaps:	0

US-10-079-954-1 (1-297) x US-09-822-827-114 (1-241)

1	GCAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGCTGCTCCAGTGCACGACG	60
:::		
33	SerIleAspGGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerSerAlaMetGin	52
:		
61	TTTGTCACGTGGGGTACTTCCTCATCGACCGGGCGTGTGTCCTTTGCTCTTTGTTTC	120
:		
53	PheValAenValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe	72
:		
121	CTGGCGTCTATGTGCTTAAGACGTGAGACGAGTGTGCCCTCTGACGTTTCTTCTTCATC	180
:		
73	LeuGlyCystYrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePheIle	92
:		
181	CTCTCTCTCATCTTCATTGCTGAGGTGTCAGCTGCTGTGTCCTTGGTGGTACACCATA	240
:		
93	LeuLeuLeuIlePheIleAlaGluValAlaAlaValValAlaLeuValTyrThrThr	112
:		
241	ATGGCTGAGCACTTCCGACGCTGCTGCTAGTGCCTGCCATCAAGAAG	288
:		
113	MetalGluHisPheLeuThrLeuLeuValValProAlaIleLysIvs	128

RESULT 8

```

US-09-115-453-114
; Sequence 114, Application US/09115453B
; Patent No. US20020090372A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115,453B
; CURRENT FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-115-453-114

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Alignment Scores:		
Pred. No.:	3.35e-40	241
Score:	453.00	93
Percent Similarity:	79.9%	Conservative: 1
Best Local Similarity:	96.9%	Mismatches: 2
Query Match:	80.3%	Indels: 0
DB:	3	Gaps: 0

US-10-079-954-1 (1-297) x US-09-115-453-114 (1-241)

1 GCAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAG 60
:::
33 SerIleAspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerSerAlaMetGln 52
61 TTGTGCAACGTGGGCTACTTCTCATCCAGCCGGGTTGTGTCTTTGTCTTGTGGTTTC 120
53 PheValIleValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72
121 CTGGGCTGCTATGGTCTTAAGACTGAGACGAAGTGTGCCCTCGTGCAGTCTTCTTTCATC 180
73 LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePheIle 92
181 CTCCTCTCTCATCTTCATTTGCTGAGGTTGCAGCTGCTGTGTGTCGCCTTGGTGACACCA 240

Db	93	LeuLeuLeuLeuPheIleAlaGluValAlaAlaValAlaLeuValTyrThrThr	112
QY	241	ATGGCTGAGCACTTCCCGACGTTGCTGGTAGTCCCTGCCATCAAGAAG	288
Db	113	MetAlaGluHisPheLeuThrLeuLeuValProAlaIleLysLys	128

RESULT 9

```

US-09-232-880-114
; Sequence 114, Application US/09232880
; Publication No. US20020182596A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C6
; CURRENT APPLICATION NUMBER: US/09/232,880
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-232-880-114

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Alignment Scores:		
Pred. No.:	3.35e-40	Length:
Score:	453.00	Matches:
Percent Similarity:	96.9%	Conservative:
Best Local Similarity:	96.9%	Mismatches:
Query Match:	80.3%	Indels:
DB:	3	Gaps:

US-10-079-954-1 (1-297) x US-09-232-880-114 (1-241)

1	GCATCATGATGGGCGATCCTTTCTGAAAGATCTTCTGGGGCCACTGTCGTCAGTGCCTCATGGAG	60
33	SerIleAspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerAlaMetGln	52
61	TTTGTCAACGTGGGCTACTTCCTCATCGACGGGGTGTGTCTTTGTCTCTCTGGTTTC	120
53	PheValAsnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe	72
121	CTGGGCTGCTATGGTGTCTAAGACTGAGAGCAAGTGTGCCCTCGTAGCGTCTCTTCTTCATC	180
73	LeuGlyCysTyrGlyAlaIysThrGluSerLysCysAlaLeuValThrPhePhePheIle	92
181	CTCTCTCTCATCTTCATGTGTGAGGTTGCGAGCTGCTGTGCGCTGTGGTGACACCATA	240
93	LeuLeuLeuIlePheIleAlaGluAlaAlaAlaValAlaLeuValTyrThrThr	112
241	ATGGCTGAGCACTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAAG	288
113	MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLeuLys	128

RESULT 10

US-09-908-193-44
; Sequence 44, Application US/09908193
; Publication No. US20020192748A1
; GENERAL INFORMATION:
; APPLICANT: RASTELLI, LUCA
; APPLICANT: SHIMKETS, RICHARD A.
; APPLICANT: ZERKHUSEN, BRYAN
; APPLICANT: MALYANKAR, URIEL M.
; APPLICANT: PADIGARU, MURALIDHARA
; TITLE OF INVENTION: NOVEL POLYNUCLE
; FILE REFERENCE: 21402-062
; CURRENT APPLICATION NUMBER: US/09/908-193-44
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/220,272
; PRIOR FILING DATE: 2000-07-24

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:29:14 ; Search time 21.929 Seconds
(without alignments)
1190.162 Million cell updates/sec

Title: US-10-079-954-1

Perfect score: 564

Sequence: 1 gcaatgatgggcatcctt.....ccatcaagaagatttggtt 297

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0

Maximum Match 100%

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/abs/ABSSWEB_spool/US1007954/runat_23032006_102927_1781/app_query.fasta_1
-DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=Blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02p
-USER=US1007954 @CGN 1.1 476 @runat_23032006_102927_1781 -NCPUs=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A_Geneseq 21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	484	85.8	99	2 AAW47275	AAW47275 Human HPK
2	453	80.3	214	8 ADR65994	ADR65994 Human pro
3	453	80.3	214	8 ADR66892	ADR66892 Human pro
4	453	80.3	233	2 AAW75060	AAW75060 Human sec
5	453	80.3	233	6 ABO01936	ABO01936 Novel hum
6	453	80.3	233	9 ADZ12337	ADZ12337 Human sec
7	453	80.3	240	4 AAG62153	AAG62153 Human P50
8	453	80.3	241	2 AAW69386	AAW69386 Prostate
9	453	80.3	241	2 AAW59954	AAW59954 Amino aci

10	453	80.3	241	2 AAW71870	AAW71870 Amino aci
11	453	80.3	241	2 AAW58380	AAW58380 Human sec
12	453	80.3	241	3 AAY82003	AAY82003 Human imm
13	453	80.3	241	3 ABG94412	ABG94412 Human pro
14	453	80.3	241	4 AAM01118	AAM01118 Human pro
15	453	80.3	241	4 AAU69764	AAU69764 Human pro
16	453	80.3	241	4 AAB74801	AAB74801 Prostate
17	453	80.3	241	4 AAG99003	AAG99003 Human pro
18	453	80.3	241	4 ABU71654	ABU71654 Prostate
19	453	80.3	241	4 AAB90679	AAB90679 Human AR4
20	453	80.3	241	4 AAU04982	AAU04982 Human pro
21	453	80.3	241	5 ABG96434	ABG96434 Human ova
22	453	80.3	241	5 ABB95223	ABB95223 Human N1-
23	453	80.3	241	5 ABG76666	ABG76666 Prostate
24	453	80.3	241	6 ABR54335	ABR54335 Prostate
25	453	80.3	241	7 ADB75601	ADB75601 Prostate
26	453	80.3	241	7 ADB13584	ADB13584 Human pro
27	453	80.3	241	7 ADG25980	ADG25980 Human pro
28	453	80.3	241	7 ADN39286	ADN39286 Cancer/an
29	453	80.3	258	5 ABG96433	ABG96433 Human ova
30	453	80.3	258	7 ADB75599	ADB75599 Prostate
31	453	80.3	273	2 AAW61618	AAW61618 Clone HPW
32	453	80.3	273	7 ABW01500	ABW01500 Human rec
33	436.5	77.4	240	5 ABB98431	ABB98431 Human HPW
34	401	71.1	121	5 ABB89113	ABB89113 Human pol
35	396	70.2	156	8 ADB50975	ADB50975 Cancer re
36	396	70.2	156	8 ADB50970	ADB50970 Cancer re
37	365	64.7	103	5 ABP32558	ABP32558 Human gly
38	358	63.5	126	2 AAY35991	AAY35991 Extended
39	358	63.5	126	8 ADP19299	ADP19299 Human sec
40	357.5	63.4	241	5 ABB09512	ABB09512 Human TSP
41	357.5	63.4	241	8 AD010063	AD010063 Novel hum
42	353.5	62.7	207	8 ADB750972	ADB750972 Cancer re
43	346	56.0	101	2 AAY13159	AAY13159 Human sec
44	315	55.9	108	2 AAY11883	AAY11883 Human 5'

ALIGNMENTS

RESULT 1

AAW47275

ID AAW47275 standard; protein; 99 AA.

XX AAW47275;

XX 02-JUL-1998 (first entry)

XX Human HPK-1A C4.8 protein.

XX Cervical cancer; treatment; diagnosis; passage cell; lesion;

XX human foreskin keratinocyte cell line; HPK-1A; antibody; smear.

XX Homo sapiens.

XX DE19649207-C1.

XX 26-FEB-1998.

XX 27-NOV-1996; 96DE-01049207.

XX 27-NOV-1996; 96DE-01049207.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Duerst M, Nees M;

XX WPI; 1998-121623/12.

XX N-PSDB; AAV15588.

XX Nucleic acid characteristic of late or early passage cells immortalised by papilloma virus - and related polypeptide(s) and antibodies, used for diagnosis and treatment of cervical cancer and assessing potential for


```
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056633P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056639P.
PR 22-AUG-1997; 97US-0056642P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 07-MAR-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057761P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
DR WFI; 1998-609887/51.
DR N-PSDB; AAV34157.
XX
XX New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
PS Claim 1; Page 281-282; 447pp; English.
XX
XX This sequence represents a secreted human protein encoded by the gene
XX clone detailed in the descriptor line. The gene can be used to generate
XX fusion proteins by linking to the gene to a human immunoglobulin Fc
XX portion (e.g. AAV34145) for increasing the stability of the fused protein
XX as compared to the human protein only. The invention relates to 70 novel
XX genes and their fragments (nucleic acid sequences: AAV34154-V34276; amino
XX acid sequences AAV75057-W75179) which are useful for preventing, treating
XX or ameliorating medical conditions e.g. by protein or gene therapy. Also,
XX pathological conditions can be diagnosed by determining the amount of the
XX new polypeptides in a sample or by determining the presence of mutations
XX in the new polynucleotides. Specific uses are described for each of the
XX 70 polynucleotides, based on which tissues they are most highly expressed
XX in (see AAV34154 for described uses). (Updated on 25-MAR-2003 to correct
XX PF field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 233 AA;
Alignment Scores:
Pred. No.: 1,55e-45 Length: 233
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 2 Gaps: 0
US-10-079-954-1 (1-297) x AAV75060 (1-233)
Qy 1 GCAATCGATGGGCATCTTTCTGAGATCTTCGGGCACCTGCTCGATGCCATGCAG 60
Db 24 SerileAspGlyAlaSerPheLeuLysPheGlyProLeuSerSerAlaMetGln 43
Qy 61 TTGTCAACGTGGCTACTTCCTCATCGACCGCGCTTGTGCTTTGTCTTGGTTTC 120
Db 44 PheValAsnValGlyTyrPheLeuIleAlaAlaGlyValValValPheAlaLeuGlyPhe 63
Qy 121 CTGGCTGCTATGGTGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGAAGTCTTCTTCATC 180
```


[illegible]

KW Human; mouse; immunotherapy; cancer; leukaemia; WTI; Wilm's tumour gene;
KW chromosome 11p13; zinc finger transcription factor.

OS Homo sapiens.

PN WO200125273-A2.

XX 12-APR-2001.

XX 04-OCT-2000; 2000WO-US027465.

XX 04-OCT-1999; 99US-0157459P.

XX (CORI-) CORIXA CORP.

XX Skelky YAW, Xu J, Cheever MA, Reed SG;

XX WPI; 2001-328324/34.

XX Polypeptide comprising part of the Wilm's Tumor gene product sequence is
PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
PT and cancer associated with WTI.

PS Disclosure; Page 223-224; 228pp; English.

XX The present invention describes compositions comprising peptides derived
CC from the Wilm's tumour protein WTI and methods for their use in treating
CC malignant diseases. Peptides derived from both the murine and human WTI
CC proteins are provided. The human WTI gene is found on chromosome 11p13,
CC and the protein was shown to be a zinc finger transcription factor. The
CC immunogenic peptides of the invention are particularly useful in the
CC diagnosis and treatment of cancer and leukemia. The present sequence is
CC a polypeptide described in the exemplification of the invention

XX Sequence 240 AA;

Alignment Scores:
Pred. No.: 1,566-45 Length: 240
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 4 Gaps: 0

US-10-079-954-1 (1-297) x AAG62153 (1-240)

QY 1 GCAATCGATGGGCGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAG 60
:::|||||
Db 33 SerileaspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerAlaMetGln 52

QY 61 TTTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTGGTCTTGGCTCTTGGTTTC 120
|||||
Db 53 PheValasnValGlyTyrrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72

QY 121 CTGGCTGCTATGGTCTTAAGACTCAGACGAAGTGTGCTCGTGCCTCTTCTTCATC 180
|||||
Db 73 LeuGlyCysTyrrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe 92

QY 181 CTCCTCTCATCTTCATTTGCTGAGGTTGCAGCTGCTGTGGTGCCTTGGTGTACACCATA 240
|||||
Db 93 LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaLeuValTyrrThrThr 112

QY 241 ATGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAAG 288
|||||

Db 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

RESULT 8

AAW69386

ID AAW69386 standard; protein; 241 AA.

AC AAW69386;

XX 25-MAR-2003 (revised)

DT 08-DEC-1998 (first entry)
XX Prostate tumour specific gene clone N1-1862 protein.
XX Prostate tumour specific gene; human; prostate cancer; detection;
KW therapy.
XX Homo sapiens.

XX WO9837418-A2.

XX 27-AUG-1998.

XX 25-FEB-1998; 98WO-US003690.

XX 25-FEB-1997; 97US-00806596.

XX 01-AUG-1997; 97US-00904809.

XX 09-FEB-1998; 98US-00020747.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC;

XX WPI; 1998-480805/41.

XX N-PSDB; AAV58587.

XX Novel human prostate specific tumour protein and fragments - useful for
PT detecting and treating prostate cancers.

PS Example 1; Page 89-90; 141pp; English.

XX This sequence is encoded by a human prostate tumour specific gene, and
CC can be used in the method of the invention. The method is for detecting
CC prostate cancer comprising contacting a biological sample with an agent
CC able to bind an immunogenic portion of a prostate protein (such as this
CC protein sequence). An antibody which binds to an immunogenic portion of
CC the prostate protein, and the method can be used to detect, monitor
CC progression of, or treat prostate cancers. The antibody may also be
CC conjugated to a therapeutic agent for use in therapy of prostate cancers.
CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 241 AA;

Alignment Scores:
Pred. No.: 1,566-45 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 2 Gaps: 0

US-10-079-954-1 (1-297) x AAW69386 (1-241)

QY 1 GCAATCGATGGGCGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAG 60
:::|||||

Db 33 SerileaspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerAlaMetGln 52

QY 61 TTTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTGGTCTTGGCTCTTGGTTTC 120
|||||

Db 53 PheValasnValGlyTyrrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72

QY 121 CTGGCTGCTATGGTCTTAAGACTCAGACGAAGTGTGCTCGTGCCTCTTCTTCATC 180
|||||

Db 73 LeuGlyCysTyrrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe 92

QY 181 CTCCTCTCATCTTCATTTGCTGAGGTTGCAGCTGCTGTGGTGCCTTGGTGTACACCATA 240
|||||

Db 93 LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaLeuValTyrrThrThr 112

QY 241 ATGGCTGAGCACTTCCCGACGTTGCTGTAGTGCCTGCCATCAAGAAG 288
|||||

Db 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

Db 33 SerileaspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerSerAlaMetGln 52
 Qy 61 TTTGTCAAGTGGGCTACTTCTCATCGCAGCCGGCGTGTGGCTTTGGCTTTGGTTTC 120
 Db 53 PheValasnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72
 Qy 121 CTGGCTGCTATGGCTTAAGACTGAGAGCAAGTGTGCCCTCGTACGTTCTTCTTCATC 180
 Db 73 LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe 92
 Qy 181 CTCTCTCTCATCTTCTGAGGTTCAGCTGTGTGGCTGTGGCTGTGTACACCATTA 240
 Db 93 LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaValValValThrThr 112
 Qy 241 ATGGCTGAGCACTTCCGACGCTTGTGCTGTAGTGTGCTGCCATCAAGAAG 288
 Db 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

RESULT 11
 AAW58380
 ID AAW58380 standard; protein; 241 AA.
 XX AC AAW58380;
 XX DT 14-SEP-1998 (first entry)
 XX DE Human secreted protein AR415_4.
 XX KW AR415_4; secreted protein; protein factor; human.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Peptide 14..26
 FT /note= "putative leader/signal peptide or transmembrane
 FT domain"
 FT Protein 27..241
 FT /label= Mat_protein
 XX WO9817687-A2.
 XX PD 30-APR-1998.
 XX PF 24-OCT-1997; 97WO-US019590.
 XX PR 25-OCT-1996; 96US-00740274.
 XX PR 24-OCT-1997; 97US-00740274.
 XX PA (GENY) GENETICS INST INC.
 XX PI Jacobs K, McCooy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
 PI Spaulding V, Agostino MJ;
 XX WPI: 1998-261426/23.
 XX DR N-PSDB; AAV30916.
 XX PT Nucleic acid encoding secreted protein from human cells - useful, e.g. as
 PT immuno-modulators, anti-tumour agents, promoters of tissue growth,
 PT haemostatic and thrombolytic agents etc.
 XX PS Claim 8; Page 67-68; 114pp; English.
 XX CC This polypeptide, designated AT415_4, is a novel human secreted protein.
 CC Its amino acid sequence was deduced from a full-length AT415_4 cDNA clone
 CC (see AAV30916) isolated from a human adult retina cDNA library. The
 CC predicted amino acid sequence shows homology to human AAM35252 and CO-029
 CC tumour associated antigens, and computer predictions suggest a potential
 CC transmembrane domain centered around amino acid 100 of the protein. 11
 CC Novel human secreted proteins (see AAW58380-90) are claimed. These can be
 CC expressed in recombinant host cells for analysis, characterisation,
 CC diagnostic or therapeutic use. They can also be used as tissue or mol.wt.
 CC markers, to generate antibodies, and in interaction trap assays. They may
 CC have biological activities, e.g. cytokine, immunomodulator,

CC haematopoiesis regulating activity, tissue growth activity, activin or
 CC inhibin activity, chemotactic or chemokinetic activity, haemostatic and
 CC thrombolytic activity, receptor/ligand activity, antiinflammatory,
 CC cadherin and tumour invasion suppressor activity, and tumour inhibition
 CC activity. The proteins can be expressed in vivo from DNA, introduced in
 CC gene therapy vectors
 XX SQ Sequence 241 AA;
 Alignment Scores:
 Pred. No.: 1.56e-45 Length: 241
 Score: 453.00 Matches: 93
 Percent Similarity: 97.9% Conservative: 1
 Best Local Similarity: 96.9% Mismatches: 2
 Query Match: 80.3% Indels: 0
 DB: 2 Gaps: 0
 US-10-079-954-1 (1-297) x AAW58380 (1-241)
 Qy 1 GCATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCCATGCAG 60
 Db 33 SerileaspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerSerAlaMetGln 52
 Qy 61 TTTGTCAAGTGGGCTACTTCTCATCGCAGCCGGCGTGTGGCTTTGGCTTTGGTTTC 120
 Db 53 PheValasnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72
 Qy 121 CTGGCTGCTATGGCTTAAGACTGAGAGCAAGTGTGCCCTCGTACGTTCTTCTTCATC 180
 Db 73 LeuGlyCysTyrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe 92
 Qy 181 CTCTCTCTCATCTTCTGAGGTTCAGCTGTGTGGCTGTGGCTGTGTACACCATTA 240
 Db 93 LeuLeuLeuIlePheIleAlaGluValAlaAlaValAlaLeuValThrThr 112
 Qy 241 ATGGCTGAGCACTTCCGACGCTTGTGCTGTAGTGTGCTGCCATCAAGAAG 288
 Db 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128

RESULT 12
 AAY82003
 ID AAY82003 standard; protein; 241 AA.
 XX AC AAY82003;
 XX DT 13-JUN-2000 (first entry)
 XX DE Human immunogenic prostate tumour protein sequence SEQ ID NO:114.
 XX KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
 KW immunogenic; cytostatic; vaccine.
 XX OS Homo sapiens.
 XX WO200004149-A2.
 XX PD 27-JAN-2000.
 XX PF 14-JUL-1999; 99WO-US015838.
 XX PR 14-JUL-1998; 98US-00115453.
 XX PR 14-JUL-1998; 98US-00116134.
 XX PR 23-SEP-1998; 98US-00159812.
 XX PR 23-SEP-1998; 98US-00159822.
 XX PR 15-JAN-1999; 99US-00232149.
 XX PR 15-JAN-1999; 99US-00232880.
 XX PR 09-APR-1999; 99US-00288946.
 XX (CORI-) CORIXA CORP.
 XX Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;
 XX WPI: 2000-171268/15.
 XX DR

XX 19-JUL-2001.
PD 16-JAN-2001; 2001WO-US001574.
XX 14-JAN-2000; 2000US-00483672.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX WPI; 2001-425973/45.
DR New polynucleotide encoding a prostate-specific protein, for diagnosing,
XX monitoring and treating prostate cancer in a patient and for use in
XX vaccines.
PS Claim 2; Page 268-269; 543pp; English.
XX The present invention describes polynucleotide sequences (I) which encode
XX prostate-specific proteins (II). (I) and (II) have cytostatic activity,
XX and can be used in vaccine production and gene therapy. (I). (II),
XX antibodies to (II), fusion proteins comprising (II), and isolated T cells
XX prepared using (I) or (II) are used treat cancer in a patient. (I) and
XX the antibodies are also used in the detection of cancer in a patient. The
XX cancer that is diagnosed or treated is particularly prostate cancer. (I)
XX and (II) can be used in vaccines. The antibodies or (I) can be used for
XX monitoring the progression of cancer in a patient. (I) and (II) can also
XX be used to improve diagnostic and therapeutic methods for prostate
XX cancer. They can indicate the level of metastasis as well as the prostate
XX volume. AAH93357 to AAH93944 and AA01115 to AA01318 represent
XX polynucleotide and amino acid sequences used in the exemplification of
XX the present invention
SQ Sequence 241 AA;
Alignment Scores:
Pred. No.: 1.56e-45 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 4 Gaps: 0
US-10-079-954-1 (1-297) x AA01118 (1-241)
QY 1 GCAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCTCCAGTGCATGCAG 60
DB 33 SerileAspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerSerAlaMetGln 52
QY 61 TTTGTCAACGTGGGTACTTCTCATCGCAGCCGGCTGTGTGCTTTTGTCTTCTTGGTTTC 120
DB 53 PheValAsnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72
QY 121 CTGGCTCTATGTGCTTAAGACTGAGAGAGTGTGCTCGTGCATGCTTCTTCTATC 180
DB 73 LeuGlyCystrGlyAlaLysThrGluSerLysCysAlaLeuValThrPhePhePhe 92
QY 181 CTCTCTCCATCTTCATGCTGAGGTTCAGCTGCTGTGTGCTGTGTGTGTGTGTGTGTGTGT 240
DB 93 LeuLeuLeuIlePheIleAlaGluValAlaAlaAlaValAlaValAlaValValThrThr 112
QY 241 ATGGCTGAGCACTTCCCGACGT 288
DB 113 MetAlaGluHisPheLeuThrLeuLeuValValProAlaIleLysLys 128
RESULT 15
AAU69764
ID AAU69764 standard; protein; 241 AA.
XX
AC AAU69764;

XX 30-JAN-2002 (first entry)
XX Human prostate cDNA encoded protein #4.
XX Human; prostate cancer; cytostatic; immunostimulant; tumour; immunogen.
XX Homo sapiens.
XX WO200173032-A2.
PD 04-OCT-2001.
XX 27-MAR-2001; 2001WO-US009919.
XX 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 13-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI; 2001-639232/73.
DR N-PSDB; AAS63558.
XX New human prostate-specific polypeptides and polynucleotides useful for
XX the diagnosis and treatment of cancer, especially prostate cancer.
PT Claim 2; Page 270-271; 579pp; English.
XX The invention relates to isolated prostate-specific polynucleotides,
XX polypeptides, fusion proteins of the polypeptides, antibodies raised
XX against the polypeptides (or antigenic epitopes derived from them) and
XX antigen-presenting cells expressing the polypeptides. The antibodies are
XX useful for detecting the presence of cancer, especially prostate cancer.
XX The polypeptides, polynucleotides and the antigen-presenting cells are
XX useful for stimulating and/or expanding T cells specific for a tumour
XX protein, and for inhibiting the development of cancer especially prostate
XX cancer. Compositions comprising the polynucleotide and/or polypeptide are
XX useful for stimulating an immune response, and for treating cancer. The
XX oligonucleotide is useful for detecting cancer. The present sequence is a
XX prostate specific polypeptide of the invention
SQ Sequence 241 AA;
Alignment Scores:
Pred. No.: 1.56e-45 Length: 241
Score: 453.00 Matches: 93
Percent Similarity: 97.9% Conservative: 1
Best Local Similarity: 96.9% Mismatches: 2
Query Match: 80.3% Indels: 0
DB: 4 Gaps: 0
US-10-079-954-1 (1-297) x AAU69764 (1-241)
QY 1 GCAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCTCCAGTGCATGCAG 60
DB 33 SerileAspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerSerAlaMetGln 52
QY 61 TTTGTCAACGTGGGTACTTCTCATCGCAGCCGGCTGTGTGCTTTTGTCTTCTTGGTTTC 120
DB 53 PheValAsnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe 72

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Result No.	Score	Query Match	Length	DB	ID	Description	
1	297	100.0	297	3	US-09-308-984-1	Sequence 1, Appli	
2	282.8	95.2	933	3	US-08-808-148-2	Sequence 2, Appli	
3	282.8	95.2	1289	3	US-09-020-956-111	Sequence 111, App	
4	282.8	95.2	1289	3	US-09-030-607-111	Sequence 111, App	
5	282.8	95.2	1289	3	US-09-439-313-111	Sequence 111, App	
6	282.8	95.2	1289	3	US-09-352-616A-111	Sequence 111, App	
7	282.8	95.2	1289	3	US-09-232-149A-111	Sequence 111, App	
8	282.8	95.2	1289	3	US-09-159-812-111	Sequence 111, App	
9	282.8	95.2	1289	3	US-09-636-215-111	Sequence 111, App	
10	282.8	95.2	1289	3	US-09-685-166A-111	Sequence 111, App	
11	282.8	95.2	1289	3	US-09-115-453-111	Sequence 111, App	
12	282.8	95.2	1289	3	US-09-688-483-111	Sequence 111, App	
13	282.8	95.2	1289	3	US-09-679-426-111	Sequence 111, App	
14	282.8	95.2	1289	3	US-09-759-143-111	Sequence 111, App	
15	282.8	95.2	1289	3	US-09-651-236-111	Sequence 111, App	
16	282.8	95.2	1289	3	US-09-030-606-111	Sequence 111, App	
17	282.8	95.2	1289	3	US-09-657-279-111	Sequence 111, App	
18	282.8	95.2	1289	3	US-10-012-896-111	Sequence 111, App	
19	282.8	95.2	1324	3	US-09-148-545-82	Sequence 82, Appl	
20	282.8	95.2	1324	3	US-09-621-011-82	Sequence 82, Appl	
21	282.8	95.2	1376	3	US-09-148-545-14	Sequence 14, Appl	
22	282.8	95.2	1376	3	US-09-621-011-14	Sequence 14, Appl	
23	282.8	95.2	1533	3	US-09-807-201-14	Sequence 14, Appl	
24	272.8	91.9	1740	3	US-09-020-956-17	Sequence 17, Appl	

RESULT 2

US-08-808-148-2
; Sequence 2, Application US/08808148
; Patent No. 6020478
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer
; APPLICANT: Goli, Surya
; APPLICANT: Zhang, Hong Wolfe
; TITLE OF INVENTION: NOVEL HUMAN TUMOR-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fastseq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,148
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0218 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 933 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSNOT26
; CLONE: 2187263
; US-08-808-148-2

Query Match	95.2%;	Score 282.8;	DB 3;	Length 933;
Best Local Similarity	99.3%;	Pred. No. 2.9e-74;		
Matches 284;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	2	CAATCGATGGGGCATCCCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT	61	
Db	225	CAATCGATGGGGCATCCCTTCTGAAGATCTTCGGGCCACTGTCGTCAGTGCATGCAGT	284	
Qy	62	TTGTCAACGTGGGTACTTCTCATCCAGCCGGGTGTGGTCTTTGGCTCTCGGTTC	121	
Db	285	TTGTCAACGTGGGTACTTCTCATCCAGCCGGGTGTGGTCTTTGGCTCTCGGTTC	344	
Qy	122	TGGGCTGCTATGGTGCTAAAGACTCAGAGCAAGTGCCTCGTGACAGTTCCTTCATCC	181	
Db	345	TGGGCTGCTATGGTGCTAAAGACTCAGAGCAAGTGCCTCGTGACAGTTCCTTCATCC	404	
Qy	182	TCCTCCCTCATCTTCATTGCTGAGGTTCAGCTGCTGTGGTGCCTTGGTGACACCTAA	241	
Db	405	TCCTCCCTCATCTTCATTGCTGAGGTTCAGCTGCTGTGGTGCCTTGGTGACACCTAA	464	
Qy	242	TGGGTGAGCACTCCCGACGTTGTGGTAGTGCCTGCCATCAAGAA	287	
Db	465	TGGGTGAGCACTCCCGACGTTGTGGTAGTGCCTGCCATCAAGAA	510	

RESULT 3

```

US-09-020-956-111
; Sequence III, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MAKI, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1289 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-020-956-111

```

Query Match	95.2%	Score	282.8	DB	3	Length	1289
Best Local Similarity	99.3%	Pred. No.	3.3e-74				
Matches	284	Conservative	0	Mismatches	2	Indels	0
Gaps	0						
Qy	2	CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGGCACCTGTGTCGCAGTGCATGCAGT	61				
Db	220	CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGGCACCTGTGTCGCAGTGCATGCAGT	279				
Qy	62	TTGTCAACGTGGGCTACTTCTCATCGCAGCCGGCGTTGGTCTTTGCTCTTGGTTTCC	121				
Db	280	TTGTCAACGTGGGCTACTTCTCATCGCAGCCGGCGTTGGTCTTTGCTCTTGGTTTCC	339				
Qy	122	TGGGCTGCTATGCTGTCTAAGACTGAGAGCAAGTGTGCGCTCGTGACGTTCTTCTTCATCC	181				
Db	340	TGGGCTGCTATGCTGTCTAAGACTGAGAGCAAGTGTGCGCTCGTGACGTTCTTCTTCATCC	399				
Qy	182	TCCTCTCATCTTCATTTGCTGAGGTTGCACGTGCTGTGGTGCCTGGGTGACACCATAA	241				
Db	400	TCCTCTCATCTTCATTTGCTGAGGTTGCACGTGCTGTGGTGCCTGGGTGACACCATAA	459				
Qy	242	TGGCTGAGCACTTCCCAGCCTTGCTGGTAGTGCCTGCCATCAAGAA	287				
Db	460	TGGCTGAGCACTTCCCAGCCTTGCTGGTAGTGCCTGCCATCAAGAA	505				

RESULT 4

US-09-030-607-111
; Sequence 111, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:

Query Match 95.2%; Score 282.8; DB 3; Length 1289;
Best Local Similarity 99.3%; Pred. No. 3.3e-74;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTGCTCAGTGCACGAGT 61

RESULT 5
US-09-439-313-111
; Sequence 111, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yucui

Query Match	95.2%	Score 282.8	DB 3	Length 1289
Best Local Similarity	99.3%	Pred. No. 3.3e-74		
Matches 284	Conservative 0	Mismatches 2	Indels 0	Gaps 0
QY	2	CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGT	61	
Db	220	CAATCGATGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGT	279	
QY	62	TTGTCAACGTGGGCTACTTCTCATCGAGCGCGCGTTGGCTCTTGGCTCTGGGTTTC	121	
Db	280	TTGTCAACGTGGGCTACTTCTCATCGAGCGCGCGTTGGTGGTCTTGGCTCTGGGTTTC	339	
QY	122	TGGGCTCTATGGTGTCTAAGACTCAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC	181	
Db	340	TGGGCTCTATGGTGTCTAAGACTCAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC	399	
QY	182	TCCTCCTCATCTTCATTGCTGAGTTGCGAGTGTGTGGTCGCTTGGTGACACCAATAA	241	
Db	400	TCCTCCTCATCTTCATTGCTGAGTTGCGAGTGTGTGGTCGCTTGGTGACACCAATAA	459	
QY	242	TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCCTGGCCATCAAGAA	287	
Db	460	TGGCTGAGCACTTCTCGACGTTGCTGGTAGTGCTTGCATCAAGAA	505	

Db 220 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCTCCAGTGCCATGCAGT 279
Qy 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTGTGGTCTTTGCTCTTGGTTCC 121
Db 280 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTGTGGTCTTTGCTCTTGGTTCC 339
Qy 122 TGGGCTGTATGGTGCTAAGACTGAGACAGTGTGCCCTGTGACGTTCTTCTTCATCC 181
Db 340 TGGGCTGTATGGTGCTAAGACTGAGACAGTGTGCCCTGTGACGTTCTTCTTCATCC 399
Qy 182 TCCTCCTCATCTTCATTCGAGTTGCGAGTGTGCTGTGGTGCCTTGGTGACACCAATAA 241
Db 400 TCCTCCTCATCTTCATTCGAGTTGCGAGTGTGCTGTGGTGCCTTGGTGACACCAATAA 459
Qy 242 TGGCTGAGCACTTCCCGAGTTGCTGTGGTGTGCTGTGGTGTGCTGTGGTGTGCTGTGGT 287
Db 460 TGGCTGAGCACTTCCCGAGTTGCTGTGGTGTGCTGTGGTGTGCTGTGGTGTGCTGTGGT 505

RESULT 7
US-09-232-149A-111
; Sequence 111, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 1289
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-111

Query Match 95.2%; Score 282.8; DB 3; Length 1289;
Best Local Similarity 99.3%; Pred. No. 3.3e-74;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCTCCAGTGCCATGCAGT 61
Db 220 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCTCCAGTGCCATGCAGT 279
Qy 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTGTGGTCTTTGCTCTTGGTTCC 121
Db 280 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTGTGGTCTTTGCTCTTGGTTCC 339
Qy 122 TGGGCTGTATGGTGCTAAGACTGAGACAGTGTGCCCTGTGACGTTCTTCTTCATCC 181
Db 340 TGGGCTGTATGGTGCTAAGACTGAGACAGTGTGCCCTGTGACGTTCTTCTTCATCC 399
Qy 182 TCCTCCTCATCTTCATTCGAGTTGCGAGTGTGCTGTGGTGCCTTGGTGACACCAATAA 241
Db 400 TCCTCCTCATCTTCATTCGAGTTGCGAGTGTGCTGTGGTGCCTTGGTGACACCAATAA 459
Qy 242 TGGCTGAGCACTTCCCGAGTTGCTGTGGTGTGCTGTGGTGTGCTGTGGTGTGCTGTGGT 287
Db 460 TGGCTGAGCACTTCCCGAGTTGCTGTGGTGTGCTGTGGTGTGCTGTGGTGTGCTGTGGT 505

RESULT 8
US-09-159-812-111
; Sequence 111, Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF

; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.428C5
; CURRENT APPLICATION NUMBER: US/09/159,812A
; CURRENT FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 1289
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-159-812-111

Query Match 95.2%; Score 282.8; DB 3; Length 1289;
Best Local Similarity 99.3%; Pred. No. 3.3e-74;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCTCCAGTGCCATGCAGT 61
Db 220 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGTCTCCAGTGCCATGCAGT 279
Qy 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTGTGGTCTTTGCTCTTGGTTCC 121
Db 280 TTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTGTGGTCTTTGCTCTTGGTTCC 339
Qy 122 TGGGCTGTATGGTGCTAAGACTGAGACAGTGTGCCCTGTGACGTTCTTCTTCATCC 181
Db 340 TGGGCTGTATGGTGCTAAGACTGAGACAGTGTGCCCTGTGACGTTCTTCTTCATCC 399
Qy 182 TCCTCCTCATCTTCATTCGAGTTGCGAGTGTGCTGTGGTGCCTTGGTGACACCAATAA 241
Db 400 TCCTCCTCATCTTCATTCGAGTTGCGAGTGTGCTGTGGTGCCTTGGTGACACCAATAA 459
Qy 242 TGGCTGAGCACTTCCCGAGTTGCTGTGGTGTGCTGTGGTGTGCTGTGGTGTGCTGTGGT 287
Db 460 TGGCTGAGCACTTCCCGAGTTGCTGTGGTGTGCTGTGGTGTGCTGTGGTGTGCTGTGGT 505

RESULT 9
US-09-636-215-111
; Sequence 111, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 1289
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-111
Query Match 95.2%; Score 282.8; DB 3; Length 1289;

Best Local Similarity 99.3%; Pred. No. 3.3e-74;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGCGATCTTTCTGAAGATCTTCGGGCGCACTGCTGCCAGTCCCATGCGT 61
Db 220 CAATCGATGGGCGATCTTTCTGAAGATCTTCGGGCGCACTGCTGCCAGTCCCATGCGT 279

Qy 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGCTTGTGGTCTTTGGTCTTTGGTTTCC 121
Db 280 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGCTTGTGGTCTTTGGTCTTTGGTTTCC 339

Qy 122 TGGGCTGCTATGCTGCTAAGACTGAGCAAGTGTGCCCTCGTGCAGTCTTCTTTCATCC 181
Db 340 TGGGCTGCTATGCTGCTAAGACTGAGCAAGTGTGCCCTCGTGCAGTCTTCTTTCATCC 399

Qy 182 TCCTCCCTCATCTTCATGCTGAGTTCGAGCTGCTGTGGTGGCTTGTGGTGTACACCAATAA 241
Db 400 TCCTCCCTCATCTTCATGCTGAGTTCGAGCTGCTGTGGTGGCTTGTGGTGTACACCAATAA 459

Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCCATCAAGAA 287
Db 460 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCCATCAAGAA 505

RESULT 10

US-09-685-166A-111
; Sequence 111, Application US/09685166A

; Patent No. 6630305

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqi

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedrick, Thomas S.

; APPLICANT: Carter, Darick

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C21

; CURRENT APPLICATION NUMBER: US/09/685,166A

; CURRENT FILING DATE: 2000-10-10

; NUMBER OF SEQ ID NOS: 898

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 111

; TYPE: DNA

; LENGTH: 1289

; ORGANISM: Homo sapien

US-09-685-166A-111

Query Match 95.2%; Score 282.8; DB 3; Length 1289;
Best Local Similarity 99.3%; Pred. No. 3.3e-74;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGCGATCTTTCTGAAGATCTTCGGGCGCACTGCTGCCAGTCCCATGCGT 61
Db 220 CAATCGATGGGCGATCTTTCTGAAGATCTTCGGGCGCACTGCTGCCAGTCCCATGCGT 279

Qy 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGCTTGTGGTCTTTGGTCTTTGGTTTCC 121
Db 280 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGCTTGTGGTCTTTGGTCTTTGGTTTCC 339

Qy 122 TGGGCTGCTATGCTGCTAAGACTGAGCAAGTGTGCCCTCGTGCAGTCTTCTTTCATCC 181

Db 340 TGGGCTGCTATGCTGCTAAGACTGAGCAAGTGTGCCCTCGTGCAGTCTTCTTTCATCC 399

Qy 182 TCCTCCCTCATCTTCATGCTGAGTTCGAGCTGCTGTGGTGGCTTGTGGTGTACACCAATAA 241
Db 400 TCCTCCCTCATCTTCATGCTGAGTTCGAGCTGCTGTGGTGGCTTGTGGTGTACACCAATAA 459

Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCCATCAAGAA 287
Db 460 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCCATCAAGAA 505

RESULT 11

US-09-115-453-111

; Sequence 111, Application US/09115453B

; Patent No. 6657056

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND

; FILE REFERENCE: 210121.427C4

; CURRENT APPLICATION NUMBER: US/09/115,453B

; CURRENT FILING DATE: 1998-07-14

; NUMBER OF SEQ ID NOS: 228

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 111

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-115-453-111

Query Match 95.2%; Score 282.8; DB 3; Length 1289;
Best Local Similarity 99.3%; Pred. No. 3.3e-74;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGCGATCTTTCTGAAGATCTTCGGGCGCACTGCTGCCAGTCCCATGCGT 61
Db 220 CAATCGATGGGCGATCTTTCTGAAGATCTTCGGGCGCACTGCTGCCAGTCCCATGCGT 279

Qy 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGCTTGTGGTCTTTGGTCTTTGGTTTCC 121
Db 280 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGCTTGTGGTCTTTGGTCTTTGGTTTCC 339

Qy 122 TGGGCTGCTATGCTGCTAAGACTGAGCAAGTGTGCCCTCGTGCAGTCTTCTTTCATCC 181
Db 340 TGGGCTGCTATGCTGCTAAGACTGAGCAAGTGTGCCCTCGTGCAGTCTTCTTTCATCC 399

Qy 182 TCCTCCCTCATCTTCATGCTGAGTTCGAGCTGCTGTGGTGGCTTGTGGTGTACACCAATAA 241
Db 400 TCCTCCCTCATCTTCATGCTGAGTTCGAGCTGCTGTGGTGGCTTGTGGTGTACACCAATAA 459

Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCCATCAAGAA 287
Db 460 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCCATCAAGAA 505

RESULT 12

US-09-688-489-111

; Sequence 111, Application US/09688489

; Patent No. 6664377

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

; FILE REFERENCE: 210121.427D2

; CURRENT APPLICATION NUMBER: US/09/688,489

; CURRENT FILING DATE: 2000-10-13

; NUMBER OF SEQ ID NOS: 338

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 111

; LENGTH: 1289

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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-688-489-111

Query Match 95.2%; Score 282.8; DB 3; Length 1289;
Best Local Similarity 99.3%; Pred. No. 3.3e-74; Indels 0; Gaps 0;
Matches 284; Conservative 0; Mismatches 2;

Qy 2 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACATGTCGTCACAGTCCATGCAGT 61
Db 220 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACATGTCGTCACAGTCCATGCAGT 279
Qy 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGCTTGTGGTCTTTGCTCTTGGTTCC 121
Db 280 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGCTTGTGGTCTTTGCTCTTGGTTCC 339
Qy 122 TGGGCTGCTATGGTGTAAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
Db 340 TGGGCTGCTATGGTGTAAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 399
Qy 182 TCCTCCTCATCTTCATTCGCTGAGGTTGCAGCTGCTGTGGTGGCTTGGTGTACACCAATAA 241
Db 400 TCCTCCTCATCTTCATTCGCTGAGGTTGCAGCTGCTGTGGTGGCTTGGTGTACACCAATAA 459
Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCCATCAAGAA 287
Db 460 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCCATCAAGAA 505

RESULT 13
US-09-679-426-111
; Sequence 111, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 1289
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-679-426-111

Query Match 95.2%; Score 282.8; DB 3; Length 1289;
Best Local Similarity 99.3%; Pred. No. 3.3e-74; Indels 0; Gaps 0;
Matches 284; Conservative 0; Mismatches 2;

Qy 2 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACATGTCGTCACAGTCCATGCAGT 61
Db 220 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACATGTCGTCACAGTCCATGCAGT 279
Qy 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGCTTGTGGTCTTTGCTCTTGGTTCC 121
Db 280 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGCTTGTGGTCTTTGCTCTTGGTTCC 121

RESULT 14
US-09-759-143-111
; Sequence 111, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 1289
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-111

Query Match 95.2%; Score 282.8; DB 3; Length 1289;
Best Local Similarity 99.3%; Pred. No. 3.3e-74; Indels 0; Gaps 0;
Matches 284; Conservative 0; Mismatches 2;

Qy 2 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACATGTCGTCACAGTCCATGCAGT 61
Db 220 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACATGTCGTCACAGTCCATGCAGT 279
Qy 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGCTTGTGGTCTTTGCTCTTGGTTCC 121
Db 280 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGCTTGTGGTCTTTGCTCTTGGTTCC 339
Qy 122 TGGGCTGCTATGGTGTAAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
Db 340 TGGGCTGCTATGGTGTAAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 399
Qy 182 TCCTCCTCATCTTCATTCGCTGAGGTTGCAGCTGCTGTGGTGGCTTGGTGTACACCAATAA 241
Db 400 TCCTCCTCATCTTCATTCGCTGAGGTTGCAGCTGCTGTGGTGGCTTGGTGTACACCAATAA 459
Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCCATCAAGAA 287
Db 460 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCCATCAAGAA 287
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Db 460 TGGCTGAGCACTTCCTGACGTTGCTGTAGTGTGCTGCCATCAAGAA 505

RESULT 15

US-09-651-236-111
; Sequence 111, Application US/09651236
; Patent No. 6818751

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.42718C18

; CURRENT APPLICATION NUMBER: US/09/651.236

; CURRENT FILING DATE: 2000-08-29

; NUMBER OF SEQ ID NOS: 865

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 111

; LENGTH: 1289

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-651-236-111

Query Match 95.2%; Score 282.8; DB 3; Length 1289;
Best Local Similarity 99.3%; Pred. No. 3.3e-74;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	2	CAATCGATGGGGCATCCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCCCATGCAGT	61
Db	220	CAATCGATGGGGCATCCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCCCATGCAGT	279
Qy	62	TTGTCAACGTGGGCTACTTCTCTCATCGCAGCGGGGTTGTGGTCTTTGCTCTTGGTTTCC	121
Db	280	TTGTCAACGTGGGCTACTTCTCTCATCGCAGCGGGGTTGTGGTCTTTGCTCTTGGTTTCC	339
Qy	122	TGGGCTGTATGGTGTCTAAGACTGAGAGCAAGTGGCCCTCGTGACGTTCTTCTTCATCC	181
Db	340	TGGGCTGTATGGTGTCTAAGACTGAGAGCAAGTGGCCCTCGTGACGTTCTTCTTCATCC	399
Qy	182	TCCTCCTCATCTTCATTGCTGAGGTGCGAGTGTGCTGTGGTGGCCCTTGGTGACCAATAA	241
Db	400	TCCTCCTCATCTTCATTGCTGAGGTGCGAGTGTGCTGTGGTGGCCCTTGGTGACCAATAA	459
Qy	242	TGGCTGAGCACTTCCGAGCGTTGCTGGTAGTGCCTGCCATCAAGAA	287
Db	460	TGGCTGAGCACTTCCGAGCGTTGCTGGTAGTGCCTGCCATCAAGAA	505

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Job time : 130 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
4167.187 Million cell updates/sec

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Perfect score: 297
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	297	100.0	297	2	Aav15588 Human HPK
2	282.8	95.2	513	5	Aaf93382 Lung carc
3	282.8	95.2	624	14	Acl62169 Human col
C 4	282.8	95.2	635	4	Aai29471 Colon tum
C 5	282.8	95.2	635	8	Abz33657 Human col
6	282.8	95.2	792	6	Abk29835 Colon ade
7	282.8	95.2	933	2	Aav54014 Nucleotid
8	282.8	95.2	1044	14	Aeb35193 Human Gef
9	282.8	95.2	1076	6	Abs76533 cDNA enco
10	282.8	95.2	1076	10	Adb75600 Prostate
11	282.8	95.2	1076	13	Adr25330 Breast ca
12	282.8	95.2	1076	13	Adr65868 Human pro
13	282.8	95.2	1076	13	Adr66771 Human pro
14	282.8	95.2	1077	13	Adq85081 Human tum
15	282.8	95.2	1154	6	Abs76532 cDNA enco
16	282.8	95.2	1154	10	Adb75598 Prostate
17	282.8	95.2	1278	11	Adn39285 Cancer/an
18	282.8	95.2	1288	2	Aav48113 Nucleotid
C 19	282.8	95.2	1288	10	Aad62626 DNA #4 us

20	282.8	95.2	1288	10	AAD62609	Aad62609 Human rec
21	282.8	95.2	1289	2	AAV58587	Aav58587 prostate
22	282.8	95.2	1289	2	AAV61202	Aav61202 Full leng
23	282.8	95.2	1289	3	AB571255	Ab571255 Human pro
24	282.8	95.2	1289	4	AAH93466	Aah93466 Human pro
25	282.8	95.2	1289	4	AAAG3558	Aag63558 Human pro
26	282.8	95.2	1289	4	AAH02531	Aah02531 Prostate
27	282.8	95.2	1289	4	AAH84780	Aah84780 Human pro
28	282.8	95.2	1289	4	AAF86954	Aaf86954 Human P50
29	282.8	95.2	1289	5	ACA59367	Aca59367 Prostate
30	282.8	95.2	1289	5	AAS10109	Aas10109 Human pro
31	282.8	95.2	1289	6	ABL94930	Ab194930 Human N1-
32	282.8	95.2	1289	6	ABS58639	Ab58639 Prostate
33	282.8	95.2	1289	8	ACC95094	Acc95094 Prostate
34	282.8	95.2	1289	10	ADB13561	Adb13561 Human pro
35	282.8	95.2	1289	10	ADG25977	Adg25977 Human pro
36	282.8	95.2	1290	3	AAA06350	Aaa06350 Human imm
37	282.8	95.2	1306	13	ADR44012	Adr44012 Human bre
38	282.8	95.2	1324	2	AAV34225	Aav34225 Human sec
39	282.8	95.2	1324	8	ACD08096	AcD08096 cDNA enco
40	282.8	95.2	1324	14	AD212282	Ad212282 Human sec
41	282.8	95.2	1376	2	AAV34157	Aav34157 Human sec
42	282.8	95.2	1376	8	ACD08028	AcD08028 cDNA enco
43	282.8	95.2	1376	14	AD212214	Ad212214 Human sec
44	282.8	95.2	1456	9	ADA11015	Ada11015 Human cDN
45	282.8	95.2	1533	3	AAZ95011	Aaz95011 Cancer sp

ALIGNMENTS

RESULT 1
AAV15588
ID AAV15588 standard; DNA; 297 BP.

AC AAV15588;

DT 02-JUL-1998 (first entry)

DE Human HPK-1A C4.8 DNA.

XX Cervical cancer; treatment; diagnosis; passage cell; lesion;

KW human foreskin keratinocyte cell line; HPK-1A; antibody; smear; ss.

XX Homo sapiens.

FN DE19649207-Cl.

XX 26-FEB-1998.

PF 27-NOV-1996; 96DE-01049207.

XX 27-NOV-1996; 96DE-01049207.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Duerst M, Nees M;

DR WFI; 1998-121623/12.

DR P-PSDB; AAW47275.

XX Nucleic acid characteristic of late or early passage cells immortalised by papilloma virus - and related polypeptide(s) and antibodies, used for diagnosis and treatment of cervical cancer and assessing potential for progression of cervical lesions.

PT Claim 2; Fig 1; 8pp; German.

CC This sequence, C4.8, is derived from a human papillomavirus (HPV)

CC immortalised human foreskin keratinocyte cell line HPK-1A and is

CC characteristic of late or early passage cells. This sequence is used in a

CC method for assessing the potential for progression of cervical lesions.

CC Antibodies generated against the encoded polypeptide are used for

CC diagnosis of cervical cancer and to assess potential for lesion
CC progression. Antibodies can also be used therapeutically by inhibiting
CC the polypeptide. Antisense molecules based on the nucleotide sequence are
CC used to inhibit expression of the protein. Detecting polypeptides, or
CC related RNA, characteristic of late passage cells (which are potentially
CC malignant) in cervical smears is a reliable way of assessing progression
CC potential

XX SQ Sequence 297 BP; 46 A; 79 C; 80 G; 92 T; 0 U; 0 Other;

Query Match 100.0%; Score 297; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 5e-76;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCCATGCGAG 60
Db 1 GCAATCGATGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGTCAGTGCCATGCGAG 60
Qy 61 TTTGTCAAGTGGGCTACTTCTCATCGACGCCGCTTGCTGCTTGGTTTC 120
Db 61 TTTGTCAAGTGGGCTACTTCTCATCGACGCCGCTTGCTGCTTGGTTTC 120
Qy 121 CTGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATC 180
Db 121 CTGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATC 180
Qy 181 CTCCTCCTCATCTTCATGCTGAGGTTGCACTGCTGTGCTGGCTTGGTGTACACCAT 240
Db 181 CTCCTCCTCATCTTCATGCTGAGGTTGCACTGCTGTGCTGGCTTGGTGTACACCAT 240
Qy 241 ATGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCTGCAAGAGATTATGGTT 297
Db 241 ATGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCTGCAAGAGATTATGGTT 297

RESULT 2

AAF93382
ID AAF93382 standard; cDNA; 513 BP.

AC AAF93382;

DT 21-MAY-2001 (first entry)

DE Lung carcinoma cDNA encoding SRT protein SEQ ID 203.

Human; SRT; gene therapy; gene mapping; tissue typing; ss.

OS Homo sapiens.

PN WO200107611-A2.

PD 01-FEB-2001.

PF 21-JUL-2000; 2000WO-US020006.

PR 26-JUL-1999; 99US-0145701P.

PA (GETH) GENENTECH INC.

PI Baker KP, Goddard A, Wood WI;

DR WPI; 2001-112729/12.

PT New isolated nucleic acid molecule encoding a SRT polypeptide is useful
PT for production of recombinant SRT polypeptides, gene mapping, diagnosing
PT genetic disorders and for gene therapy.

PS Claim 2; Fig 203; 663pp; English.

CC Sequences AAF93180 - AAF93743 represent polynucleotide sequences encoding
CC human SRT proteins. The cDNA sequences are isolated from various
CC different human tissue cDNA libraries. The invention relates to a method
CC for detecting cDNA encoding an SRT protein, a vector containing cDNA

CC encoding SRT, a host cell transformed with the vector, an isolated SRT
CC polypeptide, and an antibody which binds to SRT. The polynucleotide
CC sequence can be used in gene therapy and is useful in the recombinant
CC production of SRT polypeptides, as a hybridisation probe to screen
CC libraries to isolate cDNAs with sequence identity to SRT polypeptides, to
CC map the gene encoding the SRT polypeptides and analysing genetic
CC disorders, tissue typing and disease tissue detection. The SRT
CC polynucleotide sequences can be used in polymerase chain reaction,
CC screening for new therapeutic molecules and generation of antisense RNA
CC and DNA

XX SQ Sequence 513 BP; 97 A; 135 C; 129 G; 152 T; 0 U; 0 Other;

Query Match 95.2%; Score 282.8; DB 5; Length 513;
Best Local Similarity 99.3%; Pred. No. 8.1e-72;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGCATCTTCTCGAAGATCTTCGGGCCACTGTGTCAGTGCCATGCGAGT 61
Db 99 CAATCGATGGGCATCTTCTCGAAGATCTTCGGGCCACTGTGTCAGTGCCATGCGAGT 158
Qy 62 TTGTCAACGTGGGCTACTTCTCATCGACGCCGCTTGCTGCTTGGTTTC 121
Db 159 TTGTCAACGTGGGCTACTTCTCATCGACGCCGCTTGCTGCTTGGTTTC 218
Qy 122 TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
Db 219 TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 278
Qy 182 TCCTCCTCATCTTCATGCTGAGGTTGCACTGCTGTGGTGCCTTGGTGTACACCATAA 241
Db 279 TCCTCCTCATCTTCATGCTGAGGTTGCACTGCTGTGGTGCCTTGGTGTACACCATAA 338
Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCCATCAAGAA 287
Db 339 TGGCTGAGCACTTCCCGACGTTGCTGTAGTGTGCTGCCATCAAGAA 384

RESULT 3

ACL62169
ID ACL62169 standard; cDNA; 624 BP.

AC ACL62169;

DT 24-MAR-2005 (first entry)

Human colon cancer differentially expressed polynucleotide, SEQ ID:8304.

Differential expression; diagnosis; therapy; drug screening; cancer;
neoplasm; colon tumor; breast tumor; pancreas tumor; cytostatic; vaccine;
ss.

OS Homo sapiens.

PN WO2005000087-A2.

PD 06-JAN-2005.

PF 13-MAY-2004; 2004WO-US015421.

PR 03-JUN-2003; 2003US-0475872P.

PA (CHIR) CHIRON CORP.

PI Randazzo F, Moler E, Escobedo J, Garcia PD;

DR WPI; 2005-075421/08.

PT New isolated polynucleotides, which are differentially expressed in colon
PT cancer cell, useful for treating cancer, e.g. colon cancer, breast
PT cancer, or pancreatic cancer.

PS Claim 1; SEQ ID NO 8304; 97pp; English.

or a drug having similar biological activity as EGFR inhibitor, comprising providing a sample of tumor cells from a patient to be tested, and detecting in the sample the expression of genes chosen from a panel of genes (that have been correlated with sensitivity or resistance to the EGFR inhibitor) and selecting the patient as being predicted to benefit from therapeutic administration of the EGFR inhibitor, if the expression of the gene or genes in the patient's tumor cells is statistically more similar to the expression levels of the gene or genes that has been correlated with sensitivity to the EGFR inhibitor than to resistance to the EGFR inhibitor. Also included are identifying molecules that interact with the EGFR pathway to allow or enhance responsiveness to EGFR inhibitors, polynucleotides (for detecting the expression of genes that are indicative of sensitivity or resistance to gefitinib, or its agonist, or a drug having substantially similar biological activity as gefitinib, where the polynucleotides consist of at least two polynucleotides, where each polynucleotide is at least 5 nucleotides in length, and where each polynucleotide is complementary to an RNA transcript, or nucleotide derived from it, of a gene that is regulated differently in gefitinib-sensitive tumor cells as compared to gefitinib-resistant cells), antibodies (or their antigen binding fragments or peptides) for detecting the expression of genes that are indicative of sensitivity or resistance to gefitinib (or its agonist, or a drug having substantially similar biological activity as gefitinib, which antibody selectively binds to a protein encoded by a gene comprising, or expressing a transcript comprising, a nucleic acid sequence appearing as AEB35137-AEB35330, identifying a compound with the potential to enhance the efficacy of EGFR inhibitors and treating a patient suffering from cancer. The method is useful in selecting a cancer patient (especially non-small-cell lung cancer) who is predicted to benefit from therapeutic administration of an EGFR inhibitor or its agonist, or a drug having similar biological activity as EGFR inhibitor. The present sequence represents one of the 194 genes that have been correlated with sensitivity or resistance to the EGFR inhibitor.

Sequence 1044 BP; 220 A; 283 C; 266 G; 275 T; 0 U; 0 Other;

Query Match	95.2%	Score 282.8	DB 14	Length 1044
Best Local Similarity	99.3%	Pred. No. 1.1e-71		
Matches 284	Conservative 0	Mismatches 2	Indels 0	Gaps 0
Qy	2	CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGGCCACTGTCGTGCAGTGCATGCAGT	61	
Db	221	CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGGCCACTGTCGTGCAGTGCATGCAGT	280	
Qy	62	TTGTCAACGTGGGGTACTTCTCATCGAGCGCGCGTTGGTCTTTGCTCTTGTTTCC	121	
Db	281	TTGTCAACGTGGGGTACTTCTCATCGAGCGCGCGTTGGTCTTTGCTCTTGTTTCC	340	
Qy	122	TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGGCCCTCGTGACCGTTCCTTTCATCC	181	
Db	341	TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGGCCCTCGTGACCGTTCCTTTCATCC	400	
Qy	182	TCCCTCTCATCTTCAATGCTGAGGTTCGACGTGCTGTGGTGCCTTGGTGACACCAAA	241	
Db	401	TCCCTCTCATCTTCAATGCTGAGGTTCGACGTGCTGTGGTGCCTTGGTGACACCAAA	460	
Qy	242	TGGCTGAGCACTTCCCGACGTTGCTGGTGTAGTGGCTGGCCATCAAGAA	287	
Db	461	TGGCTGAGCACTTCTGACGTTGCTGGTGTAGTGGCTGGCCATCAAGAA	506	

RESULT 9

RESOLUT 3
ABS76533
ID ABS76533 standard: cDNA: 1076 BP.

XX
AC ABS76533;

DT 11-DEC-2002 (first entry)

XX DE CDNA encoding human ovarian cancer marker M328.

XX Human; ovarian cancer; marker; cancer; familial history; brain disorder;
KW central nervous system disorder; bacterial meningitis; viral meningitis;
KW central nervous system disorder; bacterial meningitis; viral meningitis;
XX

KW	Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
KW	brain herniation; inflammation; encephalitis; testicular disorder;
KW	nonbacterial granulomatous orchitis; connective tissue disorder;
KW	heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
KW	histological type; carcinogenic; ovarian cancer marker; gene; ss.
OS	Homo sapiens.
XX	
XX	WO200271928-A2.
PN	
XX	
XX	19-SEP-2002.
PD	
XX	
XX	14-MAR-2002; 2002WO-US007826.
XX	
XX	14-MAR-2001; 2001US-0276025P.
PR	
XX	14-MAR-2001; 2001US-0276026P.
PR	
XX	10-AUG-2001; 2001US-0311732P.
PR	
XX	19-SEP-2001; 2001US-0323580P.
PR	
XX	26-SEP-2001; 2001US-0324967P.
PR	
XX	26-SEP-2001; 2001US-0325102P.
PR	
XX	26-SEP-2001; 2001US-0325149P.
XX	
XX	(MILL-) MILLENNIUM PHARM INC.
PA	
XX	
XX	Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
PI	
PI	Meyers RE, Morrisey MP, Olandt PJ, Sen A, Vleby PO, Mills GB;
PI	
PI	Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;
XX	
XX	
DR	WPI: 2002-723277/78.
DR	
XX	P-PSDB; ABG96434.
XX	
XX	
PT	Assessing whether a patient is afflicted with ovarian cancer, useful in
PT	assessing the stage or progression of the disease, comprises comparing
PT	the expression level of a cancer marker in a sample from a patient and
PT	from a non cancer patient.

Disclosure: Page 445-446; 481pp; English.

The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer (e.g. patients having a familial history of ovarian cancer). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or Parkinson's disease), brain disorders (e.g. cerebral oedema, hydrocephalus or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. non-tuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with ovarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present nucleic acid sequence encodes one of the ovarian cancer markers described in the invention.

Sequence 1076 BP: 226 A: 278 C: 283 G: 289 T: 0 U: 0 Other:

Query Match	95.2%	Score 282.8;	DB 6;	Length 1076;
Best Local Similarity	99.3%;	Pred. No. 1.1e-71;		
Matches	284.	Conservative	0;	Mismatches 2;
				Indels 0;
				Gaps 0;

QY 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGTGTCCAGTGCATGCAGT 61

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	297	100.0	297	5	US-10-079-954-1	Sequence 1, Appli
2	282.8	95.2	513	5	US-10-052-283-203	Sequence 203, App
C 3	282.8	95.2	635	3	US-09-922-217-1025	Sequence 1035, Ap
	282.8	95.2	635	3	US-09-833-263-1025	Sequence 1025, Ap
C 4	282.8	95.2	635	5	US-10-025-380-1025	Sequence 1025, Ap
	282.8	95.2	635	3	US-09-878-134-361	Sequence 361, App
6	282.8	95.2	792	3	US-09-878-134-361	Sequence 361, App
7	282.8	95.2	1044	8	US-10-775-920-132	Sequence 132, App
8	282.8	95.2	1076	5	US-10-097-340-325	Sequence 325, App
9	282.8	95.2	1076	5	US-10-205-823-424	Sequence 424, App
10	282.8	95.2	1076	6	US-10-172-118-1191	Sequence 1191, Ap
11	282.8	95.2	1076	7	US-10-342-887-1191	Sequence 1191, Ap
12	282.8	95.2	1076	8	US-10-775-920-136	Sequence 136, App
13	282.8	95.2	1076	10	US-11-051-454-424	Sequence 424, App
14	282.8	95.2	1076	10	US-11-050-926-325	Sequence 325, App
15	282.8	95.2	1154	5	US-10-097-340-323	Sequence 323, App
16	282.8	95.2	1154	5	US-10-205-823-422	Sequence 422, App
17	282.8	95.2	1154	10	US-11-051-454-422	Sequence 422, App
18	282.8	95.2	1154	10	US-11-050-926-323	Sequence 323, App
19	282.8	95.2	1278	6	US-10-295-027-603	Sequence 603, App
20	282.8	95.2	1278	7	US-10-240-425-400	Sequence 400, App
21	282.8	95.2	1278	8	US-10-775-920-130	Sequence 130, App
22	282.8	95.2	1288	6	US-10-156-136-4	Sequence 4, Appli
C 23	282.8	95.2	1288	6	US-10-156-136-50	Sequence 50, Appl

C	24	282.8
	25	282.8
	26	282.8
	27	282.8
	28	282.8
	29	282.8
	30	282.8
	31	282.8
	32	282.8
	33	282.8
	34	282.8
	35	282.8
	36	282.8
	37	282.8
	38	282.8
39	282.8	
40	282.8	
41	282.8	
42	282.8	
43	282.8	
44	282.8	
45	282.8	

Db 241 ATGCTGAGCACTTCCGACGTTGCTGCTGCTGCTGCCATCAAGAGATTATGTT 297

RESULT 2

US-10-052-283-203

Sequence 203, Application US/10052283

Publication No. US20030064379A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Goddard, Audrey

APPLICANT: Wood, William I.

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND METHOD OF USE THEREOF

FILE REFERENCE: P2751R1C1

CURRENT APPLICATION NUMBER: US/10/052,283

CURRENT FILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: PCT/US00/20006

PRIOR FILING DATE: 2000-07-21

PRIOR APPLICATION NUMBER: US 60/145,701

PRIOR FILING DATE: 1999-07-26

NUMBER OF SEQ ID NOS: 564

SEQ ID NO 203

LENGTH: 513

TYPE: DNA

ORGANISM: Homo Sapien

US-10-052-283-203

Query Match 95.2%; Score 282.8; DB 5; Length 513;

Best Local Similarity 99.3%; Pred. No. 6.5e-80;

Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGCGATCCCTTTCTGAAGATCTTCGGGGCCACTGTCGTCAGTGCCTATGCAGT 61

Db 99 CAATCGATGGGCGATCCCTTTCTGAAGATCTTCGGGGCCACTGTCGTCAGTGCCTATGCAGT 158

Qy 62 TTGTCACGTGGGGTACTTCTCTCATCGCAGCGGGGTTGGTCTTTGCTCTTGGTTTCC 121

Db 159 TTGTCAACGTGGGGTACTTCTCTCATCGCAGCGGGGTTGGTCTTTGCTCTTGGTTTCC 218

Qy 122 TGGGCTGCTATGTTGCTAAGACTCAGAGCAAGTGTGCGCTCGTGACGTTCTTCTTCATCC 181

Db 219 TGGGCTGCTATGTTGCTAAGACTCAGAGCAAGTGTGCGCTCGTGACGTTCTTCTTCATCC 278

Qy 182 TCCTCCTCATCTTCATTGCTGAGGTTGCGAGTGTGCTGTGGTGCCTTGGTGTACACCAATAA 241

Db 279 TCCTCCTCATCTTCATTGCTGAGGTTGCGAGTGTGCTGTGGTGCCTTGGTGTACACCAATAA 338

Qy 242 TGGGCTGAGCACTTCCCGACGTTGCTGTAGTGGCTGCGCATCAAGAA 287

Db 339 TGGGCTGAGCACTTCCGTGAGTGTGCTGTAGTGGCTGCGCATCAAGAA 384

RESULT 3

US-09-922-217-1025/c

Sequence 1025, Application US/09922217

Patent No. US2002007641A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Lodes, Michael J.

APPLICANT: Secrist, Heather

APPLICANT: Benson, Darin R.

APPLICANT: Meagher, Madeleine Joy

APPLICANT: Stolk, John A.

APPLICANT: Wang, Tongtong

APPLICANT: Jiang, Yuqiu

APPLICANT: Smith, Carole Lynn

APPLICANT: King, Gordon E.

APPLICANT: Wang, Aijun

APPLICANT: Clapper, Jonathan D.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.471C13

CURRENT APPLICATION NUMBER: US/09/922,217

CURRENT FILING DATE: 2001-08-03

515	TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGCGTTGGTCTTTGCTCTTGTTGGTTTCC	456
Db		
122	TGGGCTGCTATGGTCTAAGACTGAGACAAAGTGTGCCCTCGTGAAGTCTTCTTCTTCATCC	181
Qy		
455	TGGGCTGCTATGGTCTAAGACTGAGACAAAGTGTGCCCTCGTGAAGTCTTCTTCTTCATCC	396
Db		
182	TCTCTCTCATCTTCAATTGCTGAGGTTGCAGCTGCTGTGGTCGCTTGGTGTACACATAA	241
Qy		
395	TCTCTCTCATCTTCAATTGCTGAGGTTGCAGCTGCTGTGGTCGCTTGGTGTACACACAA	336
Db		
242	TGGCTGAGCACTTCCGACGTTGCTGTGTAGTGCCTGCCATCAAGAA	287
Qy		
335	TGGCTGAGCACTTCTTGAAGTGTGTGTAGTGCCTGCCATCAAGAA	290
Db		

RESULT 5

US-10-025-380-1025/c
; Sequence 1025, Application US/10025380

; Publication No. US20
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.

; APPLICANT: Secretist, Heat
; APPLICANT: Benson, Darin

APPLICANT: Meagher, Madeline
APPLICANT: Stolk, John A.

APPLICANT: Wang, Tongtong
APPLICANT: Jiang, Yuqiu

;
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.

APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.

APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Fanger, Gary R.

; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick

Query Match 95.2%; Score 282.8; DB 5; Length 635;
Best Local Similarity 99.3%; Pred. No. 6.9e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGTGTAGTGCCCTGCCATCAAGAA 287
|||||
Db 335 TGGCTGAGCACATTTCCTGCAGCGTTGCTGTGTAGTGCCCTGCCATCAAGAA 290

RESULT 6

US-09-878-134-361

; Sequence 361, Application US/09878134
 ; Publication No. US20020086303A1

; GENERAL INFORMATION:
 ; APPLICANT: Meagher,

APPLICANT: King, Gordon E.
APPLICANT: Xu, Jiangchun

APPLICANT: Secrist, Heath
TITLE OF INVENTION: COMPOS

; TITLE OF INVENTION: THERAPY AND DIAGNOSIS
 ; FILE REFERENCE: 210121.532

Query Match 95.2%; Score 282.8; DB 3; Length 792;
Best Local Similarity 99.3%; Pred. No. 7.3e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0

RESULT 7

US-10-775-920-132

; Sequence 132, Application US/10775920
; Publication No. US20040175744A1

; GENERAL INFORMATION:
; APPLICANT: Mergen L

; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES
 ;
 ; TITLE OF INVENTION: OF PARTICULAR SECRET
 ;

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; TITLE OF INVENTION:  IN CERTAIN CANCERS
; FILE REFERENCE:  Mergen - 0010B

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Qy	62	TTGTCAAGCTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGGTCTTTGGTTTCC	121
Db	158	TTGTCAACAGTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGGTCTTTGGTTTCC	217
Qy	122	TGGGCTGCTATGTGGTCTAAGACTGAGACCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC	181
Db	218	TGGGCTGCTATGTGGTCTAAGACTGAGACCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC	277
Qy	182	TCCTCCTCATCTTCATTGCTGAGGTTGAGCTGCTGTGGTGCCTTGGTGACACCAATAA	241
Db	278	TCCTCCTCATCTTCATTGCTGAGGTTGAGCTGCTGTGGTGCCTTGGTGACACCAATAA	337
Qy	242	TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCCCTGCCATCAAGAA	287
Db	338	TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCCCTGCCATCAAGAA	383
RESULT 10			
US-10-172-118-1191			
; Sequence 1191, Application US/10172118			
; Publication No. US2003024374A1			
; GENERAL INFORMATION:			
; APPLICANT: Dai, Hongyue			
; APPLICANT: He, Yudong			
; APPLICANT: Linsley, Peter			
; APPLICANT: Mao, Mao			
; APPLICANT: Roberts, Chris			
; APPLICANT: Van 't Veer, Laura			
; APPLICANT: Van de Vijver, Marc			
; APPLICANT: Bernards, Rene			
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients			
; FILE REFERENCE: 9301-175-999			
; CURRENT APPLICATION NUMBER: US/10/172.118			
; CURRENT FILING DATE: 2002-06-14			
; PRIOR APPLICATION NUMBER: 60/380, 770			
; PRIOR FILING DATE: 2002-05-14			
; NUMBER OF SEQ ID NOS: 2699			
; SEQ ID NO 1191			
; LENGTH: 1076			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; PUBLICATION INFORMATION:			
; DATABASE ACCESSION NUMBER: NM_005727			
; DATABASE ENTRY DATE: 2001-06-18			
US-10-172-118-1191			
Query Match 95.2%; Score 282.8; DB 6; Length 1076;			
Best Local Similarity 99.3%; Pred. No. 86-80; 2; Indels 0; Gaps 0			
Matches 284; Conservative 0; Mismatches			
Qy	2	CAATCGATGGGCGATCCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCATGCAGT	61
Db	98	CAATCGATGGGCGATCCCTTTCTGAAGATCTTCGGGCCACTGTGCTCCAGTGCATGCAGT	157
Qy	62	TTGTCAAGCTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGGTCTTTGGTTTCC	121
Db	158	TTGTCAACAGTGGGCTACTTCTCATCGCAGCGCGGTTGTGGTCTTTGGTCTTTGGTTTCC	217
Qy	122	TGGGCTGCTATGTGGTCTAAGACTGAGACCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC	181
Db	218	TGGGCTGCTATGTGGTCTAAGACTGAGACCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC	277
Qy	182	TCCTCCTCATCTTCATTGCTGAGGTTGAGCTGCTGTGGTGCCTTGGTGACACCAATAA	241
Db	278	TCCTCCTCATCTTCATTGCTGAGGTTGAGCTGCTGTGGTGCCTTGGTGACACCAATAA	337
Qy	242	TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCCCTGCCATCAAGAA	287
Db	338	TGGCTGAGCACTTCCGACGTTGCTGGTAGTGCCCTGCCATCAAGAA	383

```

US-10-342-887-1191
; Sequence 1191, Application US/10342887
; Publication NO. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linslev, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1191
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1191

Query Match          95.2%; Score 282.8; DB 7; Length 1076;
Best Local Similarity 99.3%; Pred. No. 8e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY      2 CAATCGATGGGGCATCTTCTCTGAAGATCTTCGGGGCACATGCTCGTCAGTGCACATCACA
DB      98 CAATCGATGGGGCATCTTCTCTGAAGATCTTCGGGGCACATGCTCGTCAGTGCACATCACA
QY      62 TTGTCACAGCTGGGCTACTTCTCTCATCGCAGCCGGCGTTGTGGTCTTTGCTCTTTGGTTT
DB      158 TTGTCACAGCTGGGCTACTTCTCTCATCGCAGCCGGCGTTGTGGTCTTTGCTCTTTGGTTT
QY      122 TGGGCTGCTATGGTGCTTAAGACTGAGACGAAGTGTGCCCTCGTGACGTTCTTCTTCA
DB      218 TGGGCTGCTATGGTGCTTAAGACTGAGACGAAGTGTGCCCTCGTGACGTTCTTCTTCA
QY      182 TCCTCTCATCTTTCATTTGCTCAGGTGTCAGCTGCTGTGTGTGGCTTGGTGTACACCAT
DB      278 TCCTCTCATCTTTCATTTGCTCAGGTGTCAGCTGCTGTGTGTGGCTTGGTGTACACCAT
QY      242 TGGCTGAGACACTTCCCGACGTTGCTGTGTAGTGTGCTGCCATCAAGAA 287
DB      338 TGGCTGAGACACTTCCCGACGTTGCTGTGTAGTGTGCTGCCATCAAGAA 383

RESULT 12
US-10-775-920-136
; Sequence 136, Application US/10775920
; Publication NO. US20040175744A1
; GENERAL INFORMATION:
; APPLICANT: Merzen Ltd
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED
; TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEIN
; TITLE OF INVENTION: IN CERTAIN CANCERS
; FILE REFERENCE: Merzen - 0010B
; CURRENT APPLICATION NUMBER: US/10/775,920
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/447,900
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 385
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 136
; LENGTH: 1076
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-10-775-920-136

Query Match          95.2%; Score 282.8; DB 8; Length 1076;
Best Local Similarity 99.3%; Pred. No. 8e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCGCACTGTCGATGCCATGCGAGT 61
DB 98 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCGCACTGTCGATGCCATGCGAGT 157

QY 62 TTGTCAACGTTGGGCTACTCTCTCATCGACCGCGGTTGTGGTCTTTGGTCTTTGGTTTC 121
DB 158 TTGTCAACGTTGGGCTACTCTCTCATCGACCGCGGTTGTGGTCTTTGGTCTTTGGTTTC 217

QY 122 TGGGCTGCTATGGTGTGAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
DB 218 TGGGCTGCTATGGTGTGAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 277

QY 182 TCCTCTCATCTTCTCATCTGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 241
DB 278 TCCTCTCATCTTCTCATCTGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 337

QY 242 TGGCTGAGCACTTCCCGAGCTTGTGTAGTGCCTGCCATCAAGAA 287
DB 338 TGGCTGAGCACTTCCCGAGCTTGTGTAGTGCCTGCCATCAAGAA 383

RESULT 13
US-11-051-454-424
; Sequence 424, Application US/11051454
; Publication No. US20050191673A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsley, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/11/051,454
; PRIOR FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: US/10/205,823
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 424
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-051-454-424

Query Match          95.2%; Score 282.8; DB 10; Length 1076;
Best Local Similarity 99.3%; Pred. No. 8e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCGCACTGTCGATGCCATGCGAGT 61
DB 98 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCGCACTGTCGATGCCATGCGAGT 157

QY 62 TTGTCAACGTTGGGCTACTCTCTCATCGACCGCGGTTGTGGTCTTTGGTCTTTGGTTTC 121
DB 158 TTGTCAACGTTGGGCTACTCTCTCATCGACCGCGGTTGTGGTCTTTGGTCTTTGGTTTC 217

QY 122 TGGGCTGCTATGGTGTGAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
DB 218 TGGGCTGCTATGGTGTGAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 277

QY 182 TCCTCTCATCTTCTCATCTGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 241
DB 278 TCCTCTCATCTTCTCATCTGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 337

QY 242 TGGCTGAGCACTTCCCGAGCTTGTGTAGTGCCTGCCATCAAGAA 287
DB 338 TGGCTGAGCACTTCCCGAGCTTGTGTAGTGCCTGCCATCAAGAA 383

RESULT 14
US-11-050-926-325
; Sequence 325, Application US/11050926
; Publication No. US20050214831A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPURU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/11/050,926
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: US/10/097,340
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-050-926-325

Query Match          95.2%; Score 282.8; DB 10; Length 1076;

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Best Local Similarity 99.3%; Pred. No. 8e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGGCATCCCTTTCTGAAGATCTTGGGGCCACTGCTCCAGTGCCATGCAGT 61
Db 98 CAATCGATGGGGCATCCCTTTCTGAAGATCTTGGGGCCACTGCTCCAGTGCCATGCAGT 157

Qy 62 TTGTCAACGTGGGGCTACTTCTCATCGCAGCGGGCTTGTGGTCTTTGGTCTTGGTTTCC 121
Db 158 TTGTCAACGTGGGGCTACTTCTCATCGCAGCGGGCTTGTGGTCTTTGGTCTTGGTTTCC 217

Qy 122 TGGGCTGCTATGGTCTTAAGACTGAGACAAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
Db 218 TGGGCTGCTATGGTCTTAAGACTGAGACAAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 277

Qy 182 TCCTCTCATCTTCAATTCCTGAGGTTCAGCTGCTGTGGTTCGCTTGGTGTACACCAATAA 241
Db 278 TCCTCTCATCTTCAATTCCTGAGGTTCAGCTGCTGTGGTTCGCTTGGTGTACACCAATAA 337

Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
Db 338 TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 383

RESULT 15
US-10-097-340-323
; Sequence 323, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPURU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 323
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-323

Query Match 95.2%; Score 282.8; DB 5; Length 1154;

Best Local Similarity 99.3%; Pred. No. 8.1e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGGCATCCCTTTCTGAAGATCTTGGGGCCACTGCTCCAGTGCCATGCAGT 61
Db 221 CAATCGATGGGGCATCCCTTTCTGAAGATCTTGGGGCCACTGCTCCAGTGCCATGCAGT 280

Qy 62 TTGTCAACGTGGGGCTACTTCTCATCGCAGCGGGCTTGTGGTCTTTGGTCTTGGTTTCC 121
Db 281 TTGTCAACGTGGGGCTACTTCTCATCGCAGCGGGCTTGTGGTCTTTGGTCTTGGTTTCC 340

Qy 122 TGGGCTGCTATGGTCTTAAGACTGAGACAAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
Db 341 TGGGCTGCTATGGTCTTAAGACTGAGACAAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 400

Qy 182 TCCTCTCATCTTCAATTCCTGAGGTTCAGCTGCTGTGGTTCGCTTGGTGTACACCAATAA 241
Db 401 TCCTCTCATCTTCAATTCCTGAGGTTCAGCTGCTGTGGTTCGCTTGGTGTACACCAATAA 460

Qy 242 TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
Db 461 TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 506

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Job time : 534 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 23, 2006, 12:10:30 ; Search time 344 Seconds
(without alignments)
2013.130 Million cell updates/sec

Title: US-10-079-954-1

Perfect score: 297

Sequence: 1 gcaatcgatggggcattctt.....ccatcaagaagattatggtt 297

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA New.*
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2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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5: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2.*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3.*
12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	282.8	95.2	635	12	US-11-108-172-1025 Sequence 1025, Ap
C 2	282.8	95.2	1289	12	US-11-234-786-111 Sequence 111, App
C 3	281.8	94.9	601	12	US-11-108-172-884 Sequence 884, App
C 4	281.8	94.9	693	12	US-11-108-172-950 Sequence 950, App
C 5	280.8	94.5	649	12	US-11-108-172-925 Sequence 925, App
C 6	278	93.6	471	5	US-09-978-360A-198 Sequence 198, App
C 7	272.8	91.9	740	12	US-11-234-786-17 Sequence 17, App
C 8	263.8	88.8	729	12	US-11-234-786-13 Sequence 13, App
C 9	232	78.1	479	12	US-11-108-172-472 Sequence 472, App
C 10	220.6	74.3	801	12	US-11-234-786-16 Sequence 16, App
C 11	194.8	65.6	762	12	US-11-019-711-21 Sequence 21, App
C 12	191.6	64.5	751	12	US-11-234-786-12 Sequence 12, App
C 13	70.8	23.8	2942	12	US-11-000-688-1103 Sequence 1103, App
C 14	56.6	19.1	1400	12	US-11-136-527-6335 Sequence 6335, App
C 15	56.6	19.1	1497	12	US-11-136-527-2239 Sequence 2239, App
C 16	51	17.2	566	7	US-10-475-075-636 Sequence 636, App
C 17	51	17.2	687	8	US-10-821-234-414 Sequence 414, App
C 18	51	17.2	1120	8	US-10-276-233A-8 Sequence 8, App
C 19	51	17.2	1246	12	US-11-000-688-678 Sequence 678, App
C 20	49.2	16.6	1151	12	US-11-136-527-3351 Sequence 3351, App

21	49.2	16.6	1151	12	US-11-136-527-7447	Sequence 7447, App
22	48.8	16.4	863	8	US-10-453-372-463	Sequence 463, App
23	48.8	16.4	865	8	US-10-453-372-461	Sequence 461, App
24	48.8	16.4	1622	7	US-10-329-258-24	Sequence 24, Appl
25	48.8	16.4	1624	8	US-10-627-952-19	Sequence 19, Appl
26	48.8	16.4	1835	8	US-10-821-234-834	Sequence 834, App
c	46.8	15.8	551	12	US-11-128-061-2774	Sequence 2774, Ap
27	46.8	15.8	551	12	US-11-128-061-6416	Sequence 6416, Ap
28	46.8	15.8	551	12	US-11-128-049-2774	Sequence 2774, Ap
29	46.8	15.8	551	12	US-11-128-049-6416	Sequence 6416, Ap
30	46.8	15.8	551	12	US-11-128-049-6416	Sequence 3050, Ap
31	46.8	15.8	1764	12	US-11-136-527-3050	Sequence 1120, Ap
32	45.4	15.3	732	12	US-11-108-172-1120	Sequence 1084, Ap
33	45.4	15.3	1035	12	US-11-108-172-1084	Sequence 1052, Ap
34	45.4	15.3	1104	12	US-11-108-172-1052	Sequence 1119, Ap
35	45.4	15.3	1341	12	US-11-108-172-1119	Sequence 83, Appl
36	43.4	14.6	933	12	US-11-136-527-83	Sequence 14, Appl
37	42.8	14.4	679	8	US-10-623-155-14	Sequence 60781, A
38	41.8	14.1	1320	8	US-10-750-185-60781	Sequence 60781, A
39	41.8	14.1	1320	8	US-10-750-623-60781	Sequence 469401,
40	41.6	14.0	664	6	US-09-925-065A-469401	Sequence 12, Appl
41	39.2	13.2	560	12	US-11-108-172-12	Sequence 283337,
c	37.4	12.6	591	6	US-09-925-065A-283337	Sequence 4440, Ap
c	37.4	12.6	1400	12	US-11-136-527-4440	Sequence 344, App
c	37.4	12.6	2305	12	US-11-136-527-344	Sequence 88, Appl
45	36.8	12.4	1829	8	US-10-947-249-88	

ALIGNMENTS

RESULT 1

US-11-108-172-1025/c
; Sequence 1025, Application US/11/108/172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C15
; CURRENT APPLICATION NUMBER: US/11/108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321

;; CURRENT FILING DATE: 2005-04-15
;; PRIOR APPLICATION NUMBER: US 10/025,380
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: US 09/922,217
;; PRIOR FILING DATE: 2001-08-03
;; PRIOR APPLICATION NUMBER: US 09/833,263
;; PRIOR FILING DATE: 2001-04-10
;; PRIOR APPLICATION NUMBER: US 09/649,811
;; PRIOR FILING DATE: 2000-08-28
;; PRIOR APPLICATION NUMBER: US 09/609,448
;; PRIOR FILING DATE: 2000-06-29
;; PRIOR APPLICATION NUMBER: US 09/575,251
;; PRIOR FILING DATE: 2000-05-19
;; PRIOR APPLICATION NUMBER: US 09/519,444
;; PRIOR FILING DATE: 2000-03-06
;; PRIOR APPLICATION NUMBER: US 09/504,629
;; PRIOR FILING DATE: 2000-02-15
;; PRIOR APPLICATION NUMBER: US 09/480,321
;; PRIOR FILING DATE: 2000-01-10
;; PRIOR APPLICATION NUMBER: US 09/476,296
;; PRIOR FILING DATE: 1999-12-30
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1130
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 884
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 555
;; OTHER INFORMATION: n = A,T,C or G
US-11-108-172-884

Query Match 94.9%; Score 281.8; DB 12; Length 601;
Best Local Similarity 99.0%; Pred. No. 1.7e-70;
Matches 283; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGCTGCCAGTCCCATGAGT 61
DB 575 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGCTGCCAGTCCCATGAGT 516
QY 62 TTGTCAACGTGGGCTACTCTCTCATCGAGCCGGGTTGGTCTTTGCTCTTGGTTTC 121
DB 515 TTGTCAACGTGGGCTACTCTCTCATCGAGCCGGGTTGGTCTTTGCTCTTGGTTTC 456
QY 122 TGGGCTGTATGGTCTTAAGACTGAGACCAAGTGTGCCCTGTGAGCTTCTTCTATCC 181
DB 455 TGGGCTGTATGGTCTTAAGACTGAGACCAAGTGTGCCCTGTGAGCTTCTTCTATCC 396
QY 182 TCCTCTCATCTTCATTCGAGGTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
DB 395 TCCTCTCATCTTCATTCGAGGTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 336
QY 242 TGGCTGAGCACTTCCCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 287
DB 335 TGGCTGAGCACTTCTCTGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 290

RESULT 4
US-11-108-172-950/c
; Sequence 950, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secret, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongcong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.

;; APPLICANT: King, Gordon E.
;; APPLICANT: Wang, Aijun
;; APPLICANT: Clapper, Jonathan D.
;; APPLICANT: Skeiky, Yasir A. W.
;; APPLICANT: Fanger, Gary R.
;; APPLICANT: Vedvick Thomas S.
;; APPLICANT: Carter, Darrick
;; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
;; FILE REFERENCE: 210121.471C15
;; CURRENT APPLICATION NUMBER: US/11108,172
;; CURRENT FILING DATE: 2005-04-15
;; PRIOR APPLICATION NUMBER: US 10/025,380
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: US 09/922,217
;; PRIOR FILING DATE: 2001-08-03
;; PRIOR APPLICATION NUMBER: US 09/833,263
;; PRIOR FILING DATE: 2001-04-10
;; PRIOR APPLICATION NUMBER: US 09/649,811
;; PRIOR FILING DATE: 2000-08-28
;; PRIOR APPLICATION NUMBER: US 09/609,448
;; PRIOR FILING DATE: 2000-06-29
;; PRIOR APPLICATION NUMBER: US 09/575,251
;; PRIOR FILING DATE: 2000-05-19
;; PRIOR APPLICATION NUMBER: US 09/519,444
;; PRIOR FILING DATE: 2000-03-06
;; PRIOR APPLICATION NUMBER: US 09/504,629
;; PRIOR FILING DATE: 2000-02-15
;; PRIOR APPLICATION NUMBER: US 09/480,321
;; PRIOR FILING DATE: 2000-01-10
;; PRIOR APPLICATION NUMBER: US 09/476,296
;; PRIOR FILING DATE: 1999-12-30
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1130
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 950
;; LENGTH: 693
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 556, 676
;; OTHER INFORMATION: n = A,T,C or G
US-11-108-172-950
Query Match 94.9%; Score 281.8; DB 12; Length 693;
Best Local Similarity 99.0%; Pred. No. 1.8e-70;
Matches 283; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGCTGCCAGTCCCATGAGT 61
DB 576 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGCCACTGCTGCCAGTCCCATGAGT 517
QY 62 TTGTCAACGTGGGCTACTCTCTCATCGAGCCGGGTTGGTCTTTGCTCTTGGTTTC 121
DB 516 TTGTCAACGTGGGCTACTCTCTCATCGAGCCGGGTTGGTCTTTGCTCTTGGTTTC 457
QY 122 TGGGCTGTATGGTCTTAAGACTGAGACCAAGTGTGCCCTGTGAGCTTCTTCTATCC 181
DB 456 TGGGCTGTATGGTCTTAAGACTGAGACCAAGTGTGCCCTGTGAGCTTCTTCTATCC 397
QY 182 TCCTCTCATCTTCATTCGAGGTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
DB 396 TCCTCTCATCTTCATTCGAGGTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 337
QY 242 TGGCTGAGCACTTCCCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 287
DB 336 TGGCTGAGCACTTCTCTGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 291

RESULT 5
US-11-108-172-925/c
; Sequence 925, Application US/11108172


```

RESULT 9
US-11-108-172-472
; Sequence 472, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Scribst, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darlick
; TITLE OF INVENTION: COMPOUNDS FOR IM
; TITLE OF INVENTION: OF COLON CANCER
; FILE REFERENCE: 210131.471C15
; CURRENT APPLICATION NUMBER: US/11/10
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,

```


Qy 242 TGGCTGACCACTCCCGACGTTGCTGCTAGTGCCTGCCATCAAGAA 287
 Db 349 TGGCTGAACAATTCCTGACACTCCCTGGTGGTGCCTGCTATCGAATA 394

RESULT 12

US-11-234-786-12/c
 ; Sequence 12, Application US/11234786
 ; Publication No. US20060024301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqiu
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedwick, Thomas S.
 ; APPLICANT: Carter, Darriack
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.
 ; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
 ; FILE REFERENCE: 210121.427C31
 ; CURRENT APPLICATION NUMBER: US/11/234,786
 ; CURRENT FILING DATE: 2005-09-23
 ; PRIOR APPLICATION NUMBER: US 09/568,857
 ; PRIOR FILING DATE: 2000-05-09
 ; PRIOR APPLICATION NUMBER: US 09/536,857
 ; PRIOR FILING DATE: 2000-05-27
 ; PRIOR APPLICATION NUMBER: US 09/483,672
 ; PRIOR FILING DATE: 2000-01-14
 ; PRIOR APPLICATION NUMBER: US 09/439,313
 ; PRIOR FILING DATE: 1999-11-12
 ; PRIOR APPLICATION NUMBER: US 09/352,616
 ; PRIOR FILING DATE: 1999-07-13
 ; PRIOR APPLICATION NUMBER: US 09/288,946
 ; PRIOR FILING DATE: 1999-04-09
 ; PRIOR APPLICATION NUMBER: US 09/232,149
 ; PRIOR FILING DATE: 1999-01-15
 ; PRIOR APPLICATION NUMBER: US 09/159,812
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: US 09/115,453
 ; PRIOR FILING DATE: 1998-07-14
 ; PRIOR APPLICATION NUMBER: US 09/030,607
 ; PRIOR FILING DATE: 1998-02-25
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 701
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 12
 ; LENGTH: 751
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(751)
 ; OTHER INFORMATION: n = A,T,C or G
 US-11-234-786-12

Query Match 64.5%; Score 191.6; DB 12; Length 751;
 Best Local Similarity 87.7%; Pred. No. 7,5e-45;
 Matches 257; Conservative 0; Mismatches 29; Indels 7; Gaps 5;
 Qy 2 CAATGATGGGCATCCCTTCGAGATCTTCGGG---CCACTGCTGCCAGTGCATGC 58
 Db 581 CAATNGATGGGCATCCCTTCGAGATCTTCGGG---CCACTGCTGCCAGTGCATGC 522
 Qy 59 -AGTTGTCAACGTGGGCT-ACCTCTCATCGACCGCGGTTGTGGTCTTTGCTCTTGG 116

Db 521 AGTTTGTCAACGNGGGTNAATTTCTTCATCGACCGGNGTGTGCTTTGNTTGG 462
 Qy 117 -TTTCTGGGCTGCTATGCTGCTAAAGCTGAGAGCAAGTGTGCCCTCGTACGCTTCTCT 175
 Db 461 TTTTCANGGGCTGNTATGCTGCTAAAGCTGAGAGCAAGTGTGCCCTCGGACGCTTCTCT 402
 Qy 176 TCATCTCTCTCTCATCTTCATTTGCTGAGCTTGCAGCTGCTGTGGTGCCTTTGGTGATCA 235
 Db 401 TCATCTCTCTCTCATCTTCATTTGCTGAGCTGCTGTGGTGCCTTTGGTGATCA 342
 Qy 236 CCATAATGGCTGAGCACTTCCC-GACGTTGCTGCTAGTGCCTGCTGCATCAAGAA 287
 Db 341 CCACAATGGCTGAGCACTTCCCCTGCTGAGCTTGTGCTAGTGCCTGCTGCATCAAGAA 289

RESULT 13

US-11-000-688-1103
 ; Sequence 1103, Application US/11000688
 ; Publication No. US20050287544A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BERTUCCI, Francois
 ; APPLICANT: HOULGATTE, Remi
 ; APPLICANT: BIRNBAUM, Daniel
 ; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
 ; FILE REFERENCE: 1423-R-03
 ; CURRENT APPLICATION NUMBER: US/11/000,688
 ; CURRENT FILING DATE: 2004-12-01
 ; PRIOR APPLICATION NUMBER: US 60/525,987
 ; PRIOR FILING DATE: 2003-12-01
 ; NUMBER OF SEQ ID NOS: 1596
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1103
 ; LENGTH: 2942
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial sequences:primer
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(2942)
 ; OTHER INFORMATION: tetraspanin similar to uroplakin
 ; OTHER INFORMATION: 1(LOC90139) gene.
 US-11-000-688-1103

Query Match 23.8%; Score 70.8; DB 12; Length 2942;
 Best Local Similarity 62.4%; Pred. No. 2e-10;
 Matches 111; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
 Qy 58 CAGTTTGTCAACGTGGGCTACTTCTCATCGACCGCGTGTGGTCTTTTGTCTCTTGGT 117
 Db 196 CTGCTCTCTACGGGCGCTATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 255
 Qy 118 TTCCTGGGCTGCTATGCTGCTAAAGCTGAGAGCAAGTGTGCCCTCGTACGCTTCTTTC 177
 Db 256 TTCCTGGGCTGCTGCGGGCGCTCCGTGAGAACAAAGTGTCTGCTGCTATTTTCTCTG 315
 Qy 178 ATCTCTCTCTCATCTTCATTTGCTGAGTTCAGCTGCTGTGGTGCCTTTGGTGATCA 235
 Db 316 TTCACTCTGATCATCTTCTTCTGGCAGAGCTCTCAGACGCCATCTCTGGGCTTCATCTTCA 373

RESULT 14

US-11-136-527-6335
 ; Sequence 6335, Application US/11136527
 ; Publication No. US20050287570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 031896-041000 (AWI01086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25

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; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6335
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1093)..(1093)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1390)..(1390)
; OTHER INFORMATION: n is a, c, g, or t
US-11-136-527-6335

```

Query Match	19.1%	Score 56.6;	DB 12;	Length 1400;
Best Local Similarity	59.0%;	Pred. No. 1.8e-06;		
Matches 95;	Conservative 1;	Mismatches 65;	Indels 0;	Gaps 0;
QY	75	CTACTTCCTCATCGCAGCGGTTGTGGCTTTGTCTCTTGGTTCTCGGGCTGCTATGG	134	
Db	311	CTACATTCICATTGCTGTGGAGCTGTCATGATGTTTGTAGGCTTCTCGGGTCTATGG	370	
QY	135	TGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCTCCTCTCATCTT	194	
Db	371	GGCCATCCAGGAGTCCACAGTGCCTGTGGGGAGCTTCTTCACITGCTTGTGATCCTGTT	430	
QY	195	CATTGCTGAGGTTGCAGCTGCTGTGGTCGCCCTTGGTGATCA	235	
Db	431	TGCTGTGAGGTAGCTGCGGGCATCTGGGGCTTTGTAAACA	471	

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RESULT 15
US-11-136-527-2239
; Sequence 2239, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2239
; LENGTH: 1497
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1190)..(1190)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1487)..(1487)
; OTHER INFORMATION: n is a, c, g, or t
US-11-136-527-2239

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	Query Match	19.1%	Score 56.6	DB 12	Length 1497
	Best Local Similarity	59.0%	Pred. NO. 1.9e-06		
	Matches	95	Conservative	1	Mismatches 65
					Indels 0
					Gaps 0
QY	75	CTATCTCTCATCGACCGCGCTTGGCTTTGTCTTTGGTTTCTGGCTGCTATGG	134		
Db	408	CTACATCTCATCTGTGTGGAGCTGTGATGATGTTGTAGGCTTCTCGGGTGCTATGG	467		
QY	135	TGCTAAGACTGAGACCAAGTGCCCTCGTGAAGTCTTCTTTCATCTCTCTCTCATCTT	194		

Db	468	GGCCATCCAGGAGTCCAGTGCCTGTGTGGGGAGTTCTTCACTTGCCTTGTGATCCTGTT	527
Qy	195	CATTGCTGAGTTGCAGCTCTCTGTGTCGCCCTTGGTGACA	235
Db	528	TGCTCTTAGGTAGCTGCGGGCATCTGGGGCTTTGTTAAACA	568

Search completed: March 23, 2006, 12:25:12
Job time : 345 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 23, 2006, 12:40:14 ; Search time 4.09839 Seconds
(without alignments)
1394.518 Million cell updates/sec

Title: US-10-079-954-1

Perfect score: 564

Sequence: 1 gcaatgatggggcctctt.....ccatcaagaattatggtt 297

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSSWEB-spool/US10079954/runat_23032006_102931_1829/app_query.fasta_1
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -DOOPCL=0 -DOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02p
-USER=US10079954 QCEN 1 1 77 @runat_23032006_102931_1829 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DRV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 80:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	453	80.3	241	2 A59262	tetraspan TSPAN-1
2	149.5	26.5	238	2 A59265	tetraspan TSPAN-4
3	146.5	26.0	219	1 A39574	leukocyte antigen
4	141	25.0	236	1 A35649	cell surface prote
5	141	25.0	236	1 A46472	cell surface prote
6	137.5	24.4	237	1 A36056	tumor-associated a
7	132	23.4	226	1 JX0221	CD9 antigen - bovi
8	131	23.2	226	1 S39262	CD9 antigen - rat
9	131	23.2	226	2 I49589	antigen - mouse
10	131	23.2	253	2 A59264	tetraspan TSPAN-3
11	130.5	23.1	219	1 A37243	hemopoietic cell s
12	130	23.0	228	1 A40402	CD9 antigen [valid
13	130	23.0	228	1 A42929	CD9 antigen - gree
14	130	23.0	282	2 T21696	hypothetical prote

15	129.5	23.0	267	1 A46493	metastasis suppres
16	129	22.9	218	1 A43522	23K integral membr
17	127.5	22.6	222	1 A59263	tetraspan TSPAN-2
18	127.5	22.6	266	2 I49561	C33/R2/IA4 - mouse
19	127	22.5	218	1 A40181	23K integral membr
20	125	22.2	238	1 I38016	melanoma-associate
21	114	20.2	238	1 JC2297	CD63 antigen - rab
22	112	19.9	238	1 A46508	CD63/ME491 antigen
23	112	19.9	238	1 S43511	CD63/ME491 antigen
24	107	19.0	194	2 T25548	hypothetical prote
25	105.5	18.7	281	1 B47629	cell surface glyco
26	105	18.6	242	2 T15361	hypothetical prote
27	104	18.4	233	2 T15620	hypothetical prote
28	103.5	18.4	245	2 A59258	tetraspan TSPAN-6
29	100.5	17.8	245	2 A59260	tetraspan TSPAN-6
30	92.5	16.4	264	2 A59261	tetraspan TSPAN-5
31	92.5	16.4	281	1 A47629	cell surface glyco
32	92	16.3	1711	2 C71625	variant-specific s
33	91	16.1	244	2 T13615	hypothetical prote
34	87	15.4	244	1 T13368	T-cell acute lymph
35	87	15.4	308	2 T24912	hypothetical prote
36	84	14.9	223	2 T26763	hypothetical prote
37	83	14.7	309	2 T34080	hypothetical prote
38	81	14.4	162	2 S70593	NADH2 dehydrogenas
39	78	13.8	208	2 T52368	homeobox protein H
40	77.5	13.7	779	2 G84561	hypothetical prote
41	77	13.7	209	2 AE3362	multiple antibioti
42	77	13.7	1992	1 S02771	myosin heavy chain
43	76.5	13.6	204	2 D91120	probable oxidoredu
44	76.5	13.6	204	2 D85965	probable oxidoredu
45	76.5	13.6	209	2 H65092	hypothetical prote

ALIGNMENTS

RESULT 1

A59262
tetraspan TSPAN-1 - human
C:Species: Homo sapiens (man)
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A59262
R:Todd, S.C.; Doctor, V.S.; Levy, S.
Biochim. Biophys. Acta 1399, 101-104, 1998
A:Title: Sequences and expression of six new members of the tetraspanin/TM4SF family.
A:Reference number: A59258; MUID:98390278; PMID:9714763
A:Accession: A59262
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-241 <TOD>
A:Cross-references: UNIPROT:O60635; UNIPARC:UPI000004EE36; GB:AF054838; NID:G2997740; PIR:
C:Genetics:
A:Gene: TSPAN-1
C:Superfamily: CD9 antigen

Alignment Scores:
Pred. No.: 2.38e-39
Score: 453.00
Percent Similarity: 97.9%
Best Local Similarity: 96.9%
Query Match: 80.3%
DB: 2

Length: 241
Matches: 93
Conservative: 1
Mismatch: 2
Indels: 0
Gaps: 0

US-10-079-954-1 (1-297) x A59262 (1-241)

Qy	1	GCATCGATGGGCATCTTCTTGAGATCTTGGGCACTCGTCCAGTCCATGCAG	60
Db	33	SerileaspGlyAlaSerPheLeuLysilePheGlyProleuSerSerAlaMetGln	52
Qy	61	TTTGTCAACGTGGGCTACTTCTCATCGACCGCGCTTGTGGTCTTGTCTTGGTTTC	120
Db	53	PheValIasnValGlyTyrPheLeuIleAlaAlaGlyValValPheAlaLeuGlyPhe	72
Qy	121	CTGGGCTGTATGGTGCTAGACTGAGACAGTGTGCGCCCTCGTGACGTTCTTCTTCATC	180

F:83-86/Domain: intracellular #status predicted <CY2>
F:187-111/Domain: transmembrane #status predicted <TM3>
F:112-194/Domain: extracellular #status predicted <EX2>
F:195-221/Domain: transmembrane #status predicted <TM4>
F:222-228/Domain: intracellular #status predicted <CY3>
F:53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.: 1,69e-05 Length: 228
Score: 130.00 Matches: 26
Percent Similarity: 68.8% Conservatives: 7
Best Local Similarity: 54.2% Mismatches: 15
Query Match: 23.0% Indels: 0
DB: 1 Gaps: 0

US-10-079-954-1 (1-297) x A40402 (1-228)

Qy 76 TACTTCTCATCGACCGCGGTGCTGCTTTGCTCTGTTCTTCTGGGCTGATGGT 135
Db 61 TyrilleuileGlyAlaGlyAlaLeuMetMetLeuValGlyPheLeuGlyCysGly 80
Qy 136 GCTAGACTGAGACGAGTGTGCGCTGCTGACGTTCTTCTTCATCTCTCTCTCATCTTC 195
Db 81 AlavalGlnGluSerGlnCysMetLeuGlyLeuPheGlyPheLeuLeuValIlePhe 100
Qy 196 ATTGCTGAGTTCAGCTGCTGTG 219
Db 101 AlalleGluilleAlaAlaAlaIle 108

RESULT 13

A42929
CD9 antigen - green monkey
N:Alternate names: 27K diphtheria toxin receptor-associated protein DRAP27
C:Species: Cercopithecus aethiops (green monkey, grivet)
C>Date: 01-Oct-1992 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C:Accession: A42929
R:Mitamura, T.; Iwamoto, R.; Umata, T.; Yomo, T.; Urabe, I.; Tsuneoka, M.; Mekada, E.
J. Cell Biol. 118, 1389-1399, 1992
A:Title: The 27-kD diphtheria toxin receptor-associated protein (DRAP27) from vero cells
ceptors on toxin-sensitive cells.
A:Reference number: A42929; MUID:92394967; PMID:1522113
A:Accession: A42929
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA

A:Residues: 1-228 <MT>
A:Cross-references: UNIPROT:P30409; UNIPARC:UPI000016C3B8; GB:D10726; NID:g218565; PIDN:
C:Superfamily: CD9 antigen

C:Keywords: glycoprotein; transmembrane protein
F:2-228/Product: CD9 antigen #status predicted <MAT>
F:2-11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-55/Domain: extracellular #status predicted <EX1>
F:56-82/Domain: transmembrane #status predicted <TM2>
F:83-86/Domain: intracellular #status predicted <CY2>
F:87-111/Domain: transmembrane #status predicted <TM3>
F:112-194/Domain: extracellular #status predicted <EX2>
F:195-221/Domain: transmembrane #status predicted <TM4>
F:222-228/Domain: intracellular #status predicted <CY3>
F:52.53/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.: 1,69e-05 Length: 228
Score: 130.00 Matches: 26
Percent Similarity: 68.8% Conservatives: 7
Best Local Similarity: 54.2% Mismatches: 15
Query Match: 23.0% Indels: 0
DB: 1 Gaps: 0

US-10-079-954-1 (1-297) x A42929 (1-228)

Qy 76 TACTTCTCATCGACCGCGGTGCTGCTTTGCTCTGTTCTTCTGGGCTGATGGT 135
Db 61 TyrilleuileGlyAlaGlyAlaLeuMetMetLeuValGlyPheLeuGlyCysGly 80

Qy 136 GCTAGACTGAGACGAGTGTGCGCTGCTGACGTTCTTCTTCATCTCTCTCATCTTC 195
Db 81 AlavalGlnGluSerGlnCysMetLeuGlyLeuPheGlyPheLeuLeuValIlePhe 100
Qy 196 ATTGCTGAGTTCAGCTGCTGTG 219
Db 101 AlalleGluilleAlaAlaAlaIle 108

RESULT 14

T21696

hypothetical protein F33C8.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T21696

R:Percy, C.

submitted to the EMBL Data Library, February 1996

A:Reference number: Z19460

A:Accession: T21696

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-282 <WIL>

A:Cross-references: UNIPROT:Q19983; UNIPARC:UPI000004EE37; EMBL:Z69790; PIDN:CAA93655.1;

A:Experimental source: clone F33C8

C:Genetics:

A:Gene: CESP:F33C8.3

A:Map position: X

A:Introns: 20/3; 51/1; 88/3; 146/3; 197/1; 235/3

C:Superfamily: CD9 antigen

Alignment Scores:

Pred. No.: 1,67e-05 Length: 282
Score: 130.00 Matches: 29
Percent Similarity: 52.6% Conservatives: 12
Best Local Similarity: 37.2% Mismatches: 29
Query Match: 23.0% Indels: 8
DB: 2 Gaps: 1

US-10-079-954-1 (1-297) x T21696 (1-282)

Qy 10 GGGGCATCTTTCGAAGATCTTCGGGCCACTGCTGCTCCAGTGCCATG----- 57
Db 28 GlyLeuGlyIleTrpLeuLeuPheAspProAlaAlaSerAspPheAlaLeuHisSer 47
Qy 58 -----CAGTTTGACACGGGCTACTTCTCTCATCGACGCGGCTGTGCTC 105
Db 48 ThrHisProGlyAlaPheArgTyrValGlyTrpPheLeuValGlyAlaGlyAlaIle 67
Qy 106 TTGCTCTTGGTTTCTGGGCTGCTATGCTGAAGACTGAGAGCAAGTGTGCCCTCGT 165
Db 68 IleLeuValGlyTyrPheGlyCysIleGlyAlaTrpLysMetAsnGlnCysAlaLeuAla 87
Qy 166 ACGTTCCTTTCATCTCTCTCTCTCATCTTCTGCTGAGGTTGACGCTGCTGTG 219
Db 88 PhePheCysCysIleLeuIleLeuAlaPhePheLeuGluLeuAlaAlaAlaVal 105

RESULT 15

A46493

metastasis suppressor KAI1 - human

N:Alternate names: cell surface glycoprotein KAI1; membrane protein R2, inducible; type

C:Species: Homo sapiens (man)

C>Date: 18-Jun-1993 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004

C:Accession: I38942; S16156; R46493

R:Dong, J.T.; Lamb, P.W.; Rinker-Schaeffer, C.W.; Vukanovic, J.; Ichikawa, T.; Isaacs, J.

Science 268, 884-886, 1995

A:Title: KAI1, a metastasis suppressor gene for prostate cancer on human chromosome 11p1

A:Reference number: I38942; MUID:95273964; PMID:7754374

A:Accession: I38942

A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-267 <RES>

A:Cross-references: UNIPROT:P27701; UNIPARC:UPI00001273AE; EMBL:U20770; NID:9806805; PIDN:

R:Gaugitsch, H.W.; Hofer, E.; Huber, N.E.; Schnabl, E.; Baumruker, T.

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
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2	282.8	95.2	518	6	CB161656	CB161656 K-EST0221
3	282.8	95.2	539	6	CD709223	CD709223 EST25750
4	282.8	95.2	542	3	BM819747	BM819747 K-EST0087
5	282.8	95.2	543	3	BM819711	BM819711 K-EST0087
6	282.8	95.2	546	6	CD700012	CD700012 EST16536
7	282.8	95.2	549	2	BE249898	BE249898 600942941
8	282.8	95.2	554	3	BM819756	BM819756 K-EST0087
9	282.8	95.2	559	5	BX480177	BX480177 DKF2p686E3
10	282.8	95.2	564	2	BG428609	BG428609 602494743
11	282.8	95.2	566	3	BM819724	BM819724 K-EST0087
12	282.8	95.2	568	3	BP261193	BP261193 BP261193
13	282.8	95.2	568	3	BP262643	BP262643 BP262643
14	282.8	95.2	571	3	BM819701	BM819701 K-EST0087
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16	282.8	95.2	573	3	BP263326	BP263326 BP263326
17	282.8	95.2	576	3	BP260827	BP260827 BP260827
18	282.8	95.2	579	6	CD701289	CD701289 EST17813
19	282.8	95.2	581	3	BP254783	BP254783 BP254783
20	282.8	95.2	581	3	BP262395	BP262395 BP262395
21	282.8	95.2	582	3	BP260782	BP260782 BP260782
22	282.8	95.2	582	3	BP261111	BP261111 BP261111

ORIGIN		Library from Southern Chinese			
Query Match	95.2%	Score 282.8;	DB 6;	Length 539;	
Best Local Similarity	99.3%;	Pred. No. 3.8e-66;			
Matches 284;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	
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ph	156	CAATCGATGGGCATCTTTTCTGAAGATCTTCGGGCCACTGTCTGCAGTCCCATGCAGT	215		

obtained cDNA vectors were used for transformation of competent cells *E. coli* Top10[®] by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 95.2%; Score 282.8; DB 3; Length 543;
Best Local Similarity 99.3%; Pred. No. 3.8e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGCGCCAGTGCATGCAGT 61
DB 246 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGCGCCAGTGCATGCAGT 305
QY 62 TTGTCAACGTGGGCTACTTCTCATCGAGCGCGGTTGGTCTTTCTTGTGTTTCC 121
DB 306 TTGTCAACGTGGGCTACTTCTCATCGAGCGCGGTTGGTCTTTCTTGTGTTTCC 365
QY 122 TGGGCTGTATGCTTAAGACTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
DB 366 TGGGCTGTATGCTTAAGACTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 425
QY 182 TCCTCTCATCTTCAATGCTGAGGTTGCGAGCTGCTGTGCGCCCTTGTGTACACCAATA 241
DB 426 TCCTCTCATCTTCAATGCTGAGGTTGCGAGCTGCTGTGCGCCCTTGTGTACACCAATA 485
QY 242 TGGCTGAGCACTTCCCGAGTGTGCTGTAGTGCCTGCCATCAAGAA 287
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RESULT 6

CD700012
LOCUS CD700012 546 bp mRNA linear EST 25-JUN-2003
DEFINITION EST16536 human nasopharynx Homo sapiens cDNA, mRNA sequence.

ACCESSION CD700012
VERSION CD700012.1 GI:32229841
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 546)
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.

FEATURES

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/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
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/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

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Best Local Similarity 99.3%; Pred. No. 3.8e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 315 TTGTCAACGTGGGCTACTTCTCATCGAGCGCGGTTGGTCTTTCTTGTGTTTCC 374
QY 122 TGGGCTGTATGCTTAAGACTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
DB 375 TGGGCTGTATGCTTAAGACTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 434
QY 182 TCCTCTCATCTTCAATGCTGAGGTTGCGAGCTGCTGTGCGCCCTTGTGTACACCAATA 241
DB 435 TCCTCTCATCTTCAATGCTGAGGTTGCGAGCTGCTGTGCGCCCTTGTGTACACCAATA 494
QY 242 TGGCTGAGCACTTCCCGAGTGTGCTGTAGTGCCTGCCATCAAGAA 287
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RESULT 7

BE249898
LOCUS BE249898 549 bp mRNA linear EST 13-JUL-2000
DEFINITION BE249898 549 bp Homo sapiens cDNA clone IMAGE:2959379 5', mRNA sequence.

ACCESSION BE249898
VERSION BE249898.1 GI:9120001
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 549)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csapbe-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"

FEATURES

source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
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/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
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ORIGIN

Query Match 95.2%; Score 282.8; DB 2; Length 549;
Best Local Similarity 99.3%; Pred. No. 3.8e-68;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 206 CAATCGATGGGCGATCCTTTCTGAAGATCTTCGGGCCACTGTGCGCCAGTGCATGCAGT 265
QY 62 TTGTCAACGTGGGCTACTTCTCATCGAGCGCGGTTGGTCTTTCTTGTGTTTCC 121

Db 234 CAATCGATGGGGCATCTTTCTGAAGATCTTTCGGGCCACTGTCGTCCAGTGCCATGCAGT 293

Qy 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGGTGTGGTCTTTGCTCTTGGTTTCC 121

Db 294 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGGTGTGGTCTTTGCTCTTGGTTTCC 353

Qy 122 TGGGCTGTATGTGTCTAAGACTGAGCAAGTGTGCCCTGTCGACGTTCTTCTTCATCC 181

Db 354 TGGGCTGTATGTGTCTAAGACTGAGCAAGTGTGCCCTGTCGACGTTCTTCTTCATCC 413

Qy 182 TCCTCTCATCTTCAATGCTGAGGTGTCAGTGTGGTGTGCCCTTGGTGTACACCATAA 241

Db 414 TCCTCTCATCTTCAATGCTGAGGTGTCAGTGTGGTGTGCCCTTGGTGTACACCATAA 473

Qy 242 TGGCTGAGCACTTCCCGAGCTTCTGTGTAGTGCCTGCCATCAAGAA 287

Db 474 TGGCTGAGCACTTCCCGAGCTTCTGTGTAGTGCCTGCCATCAAGAA 519

RESULT 10

LOCUS BG428609 564 bp mRNA linear EST 14-MAR-2001

DEFINITION 602494743F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4608394 5', mRNA sequence.

ACCESSION BG428609

VERSION BG428609.1 GI:13335115

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 564)

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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High quality sequence stop: 560.

FEATURES

Source

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/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site: 1: SfiI (ggccgcttggcc); Site: 2: SfiI (ggccattggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGCGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 95.2%; Score 282.8; DB 2; Length 564;

Best Local Similarity 99.3%; Pred. No. 3.9e-68;

Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAATCGATGGGGCATCTTTCTGAAGATCTTTCGGGCCACTGTCGTCCAGTGCCATGCAGT 61

Db 233 CAATCGATGGGGCATCTTTCTGAAGATCTTTCGGGCCACTGTCGTCCAGTGCCATGCAGT 292

Qy 62 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGGTGTGGTCTTTGCTCTTGGTTTCC 121

Db 293 TTGTCAACGTGGGCTACTTCTCATCGCAGCGGGGTGTGGTCTTTGCTCTTGGTTTCC 352

Qy 122 TGGGCTGTATGTGTCTAAGACTGAGCAAGTGTGCCCTGTCGACGTTCTTCTTCATCC 181

Db 353 TGGGCTGTATGTGTCTAAGACTGAGCAAGTGTGCCCTGTCGACGTTCTTCTTCATCC 412

Qy 182 TCCTCTCATCTTCAATGCTGAGGTGTCAGTGTGGTGTGCCCTTGGTGTACACCATAA 241

Db 413 TCCTCTCATCTTCAATGCTGAGGTGTCAGTGTGGTGTGCCCTTGGTGTACACCATAA 472

Qy 242 TGGCTGAGCACTTCCCGAGCTTCTGTGTAGTGCCTGCCATCAAGAA 287

Db 473 TGGCTGAGCACTTCCCGAGCTTCTGTGTAGTGCCTGCCATCAAGAA 518

RESULT 11

LOCUS BM819724 566 bp mRNA linear EST 06-MAR-2002

DEFINITION K-EST0087883 S18N669761 Homo sapiens cDNA clone S18N669761-20-E08 5', mRNA sequence.

ACCESSION BM819724

VERSION BM819724.1 GI:19176137

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 566)

AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongjung@mail.kribb.re.kr
Plate: 20 row: E column: 08
High quality sequence stop: 566.

FEATURES

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/clone="S18N669761-20-E08"

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/clone_lib="S18N669761"

/note="Organ: Stomach; Vector: pcNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

RESULT 14	
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LOCUS	K-EST0087855 S18N669761 Homo sapiens cDNA clone S18N669761-20-C03
DEFINITION	571 bp mRNA linear EST 06-MAR-2002
	S' RNA sequence.
ACCESSION	BM819701 GI:19176114
VERSION	EST.
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 571) Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R. and Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S. 21C Frontier Korean EST Project 2001 Unpublished (2002) Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel.: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 20 row: C column: 03 High quality sequence stop: 571. Location/Qualifiers 1..571
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
FEATURES	
SOURCE	

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FEATURES             Location/Qualifiers
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         sex="F"
         lab_host="Top10F"
         clone_lib="S18N669761"
         note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
         Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
         bacterial alkaline phosphatase (BAP) and then decapped
         with tabacco acid pyrophosphatase (TAP). The decapped
         intact mRNA was ligated with DNA-RNA linker including EcoR
         I site by treatment of T4 RNA ligase and the first strand
         cDNA was synthesized from oligo dT-selected mRNA by
         priming with dT-tailed vector. The dT-tailed vector was
         adjusted to have about 60nt. The cDNA vector was
         circularized with E. coli DNA ligase after digestion of
         EcoRI which site is also included in vector. An RNA strand
         converted to a DNA strand by Okayama-Berg method. The
         obtained cDNA vectors were used for transformation of
         competent cells E. coli Top10F by electroporation method.
         The cDNA libraries constructed by this method are
         full-length enriched cDNA library."

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Query Match									
Best Local Similarity 95.2%; Score 282.8; DB 3; Length 571;									
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
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Job time : 2441 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 23, 2006, 11:09:33 ; Search time 2131 Seconds
(without alignments)
7922.339 Million cell updates/sec

Title: US-10-079-954-1
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Sequence: 1 gcaatcgatgggcatcctt.....ccatcaagaagattatggtt 297

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5893141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb.in.*
3: gb.env.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
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8: gb.pt.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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c 13	282.8	95.2	1288	6	BD069078 Polynucle
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31	282.8	95.2	1289	6	AX140621 Sequence
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36	282.8	95.2	1324	6	BD195620 70 human
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38	282.8	95.2	1324	6	AR352675 Sequence
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40	282.8	95.2	1376	6	BD195552 70 human
41	282.8	95.2	1376	6	CQ775597 Sequence
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43	282.8	95.2	1376	6	AR650217 Sequence
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ALIGNMENTS

RESULT 1
A91802
LOCUS A91802 297 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1 from Patent WO9823775.
ACCESSION A91802
VERSION A91802.1 GI:6740681
KEYWORDS
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 297)
AUTHORS Nees, M. and Duerst, M.
TITLE DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
JOURNAL Patent: WO 9823775-A 1 04-JUN-1998;
DEUTSCHES KREBSFORSCH (DE); NEES MATTHIAS (DE)
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QY 181 CTCCTCCTCATCTTCATCTGCTGAGTTGTCAGCTGCTGTGGTCGCTTGGTGACACCATTA 240
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QY 241 ATGGCTGAGCACTTCCCGACGTTGCTGCTAGTGCCTGCCATCAAGAAGATTATGGTT 297
Db 241 ATGGCTGAGCACTTCCCGACGTTGCTGCTAGTGCCTGCCATCAAGAAGATTATGGTT 297

RESULT 2
LOCUS BD023236 297 bp DNA linear PAT 27-AUG-2002
DEFINITION DNA for evaluating progress potential of cervical diseases.
ACCESSION BD023236
VERSION BD023236.1 GI:22564459
KEYWORDS JP 2001504703-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1
REFERENCE
AUTHORS Baker, K.P., Goddard, A. and Wood, W.I.
TITLE Human polypeptides and methods for the use thereof
JOURNAL Patent: WO 0107611-A 203 01-FEB-2001;
Genentech, Inc. (US)
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Best Local Similarity 99.3%; Pred. No. 1.7e-61; Indels 0; Gaps 0;
Matches 284; Conservative 0; Mismatches 2;
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QY 122 TGGGCTCTATGTTGCTTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
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QY 182 TCCTCCTCATCTTCATTTGCTGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
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QY 242 TGGCTGAGCACTTCCCGACGTTGCTGCTAGTGCCTGCCATCAAGAA 287
Db 339 TGGCTGAGCACTTCCCGACGTTGCTGCTAGTGCCTGCCATCAAGAA 384

RESULT 4
LOCUS AX193458/c 635 bp DNA linear PAT 15-AUG-2001
DEFINITION Sequence 1025 from Patent WO0149716.
ACCESSION AX193458
VERSION AX193458.1 GI:15211409
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1
REFERENCE
AUTHORS Xu, J., Lodes, M.J., Secrist, H., Benson, D.R., Meagher, M.J.,
Stolk, J.A., King, G.E., Wang, T. and Jiang, Y.
TITLE Compounds for immunotherapy and diagnosis of colon cancer and
methods for their use
JOURNAL Patent: WO 0149716-A 1025 12-JUL-2001;
CORIXA CORPORATION (US)
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LOCUS BD023236 297 bp DNA linear PAT 27-AUG-2002
DEFINITION DNA for evaluating progress potential of cervical diseases.
ACCESSION BD023236
VERSION BD023236.1 GI:22564459
KEYWORDS JP 2001504703-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
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REFERENCE
AUTHORS Durst, M. and Ness, M.
TITLE DNA for evaluating progress potential of cervical diseases
JOURNAL Patent: JP 2001504703-A 1 10-APR-2001;
DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES EFFENTLICHEN RECHTS
COMMENT PN JP 2001504703-A/1
PF 10-APR-2001
PF 12-NOV-1997 JP 1998524127
PR 27-NOV-1996 DE 19649207.6
PI MATHIAS DURST, MATHIAS NESS
PC C12N15/09, C07K14/00, C07K16/00, C12P21/02, C12Q1/68, C12Q1/70, PC
GOIN33/574,
PC C12N15/00
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CC Topology: Linear;
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source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4e-65;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAATCGATGGGGATCCTTCTTGAAGATCTTCGGGGCACCTGTGTCAGTGCCATGCAG 60
Db 1 GCAATCGATGGGGATCCTTCTTGAAGATCTTCGGGGCACCTGTGTCAGTGCCATGCAG 60
QY 61 TTGTCAACGTGGGCTACTTCTCATCGACGCGGCTGTGGTCTTTGCTCTTGGTTTC 120
Db 61 TTGTCAACGTGGGCTACTTCTCATCGACGCGGCTGTGGTCTTTGCTCTTGGTTTC 120
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QY 181 CTCCTCCTCATCTTCATTTGCTGAGTTGCTGCTAGTGCCTGCCATCAAGAAATTATGGTT 240
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QY 241 ATGGCTGAGCACTTCCCGACGTTGCTGCTAGTGCCTGCCATCAAGAAGATTATGGTT 297
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	Best Local Similarity	99.3%;	Pred. No. 1.7e-61;		
	Matches 284;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	2	CAATCGAATGGGGCATCCCTTTCTGAAGATCTTTCGGGCCACTGTGTCAGTGCCTATGCAGT	61		
Db	575	CAATCGATGGGCATCCCTTTCTGAAGATCTTTCGGGCCACTGTGTCAGTGCCTATGCAGT	516		
QY	62	TTGTCAACGTTGGGCTACTTCTCATCGACGCGGGTGTGGTCTTTGCTCTTTGGTTTCC	121		
Db	515	TTGTCAACGTTGGGCTACTTCTCATCGACGCGGGTGTGGTCTTTGCTCTTTGGTTTCC	456		
QY	122	TGGGCTGCTATGGTGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGCTTCTTTCTCATCC	181		
Db	455	TGGGCTGCTATGGTGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGCTTCTTTCTCATCC	396		
QY	182	TCCTTCCTCATCTTTCATTGCTGAGGTTGCAGTGTGTTGGTGCCTTGGGTGACCAATAA	241		
Db	395	TCCTTCCTCATCTTTCATTGCTGAGGTTGCAGTGTGTTGGTGCCTTGGGTGACCAATAA	336		
QY	242	TGGCTGAGCACTTCCCGAGCTTGTGTGTAGTGCCTGCCATCAAGAA	287		
Db	335	TGGCTGAGCACTTCCGAGCTTGTGTGTAGTGCCTGCCATCAAGAA	290		

RESULT 5	AX379319	Sequence 361 from Patent WO0196389.	792 bp	DNA	linear	PAT 18-MAR-2002
LOCUS	AX379319					
DEFINITION	AX379319					
ACCESSION	AX379319					
VERSION	AX379319.1	GI:19575159				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;					
	Hominidae; Homo.					

REFERENCE
AUTHORS
TITLE
JOURNAL

[illegible]

QY 242 TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCCTGCAATCAAGAA 287
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Db 454 TGGCTGAGCACTTCCCTGACGTTGCTGGTAGTGCCCTGCAATCAAGAA 499

RESULT 6	BD070552	Novel human tumor-associated antigen.	933 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD070552					
DEFINITION	BD070552					
ACCESSION	BD070552.1	GI:22616155				
VERSION	JP 2001515349-A/1.					
KEYWORDS	unidentified					
SOURCE	unidentified					
ORGANISM	unclassified					

REFERENCE	1 (bases 1 to 933)
AUTHORS	Hillman,J.L. and Goli,S.K.
TITLE	Novel human tumor-associated antigen
JOURNAL	Patent: JP 2001515349-A 1 18-SEP-2001;
COMMENT	INCYTE PHARMACEUTICALS INC OS Unidentified

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Best Local Similarity 99.3%; Pred. No. 1.7e-61;
Matches 284; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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	Ov	182	TCCTCCTCATCTTTCATTGCTAGGTTGCAGCTGCTGTGGCTGGCTGGTGTCACACCATAA	241.

Qy	182	TCCTCCTCATCTTCATTCGTAGAGTTGCAGCTGCTGTGGTGCCTTGGTGTACACCAATAA	241
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Qy	242	TGGCTGAGCACTTCCCGACGTTCTGCTAGTGCCTGCCATCAAGAA	287
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RESULT 7	AF133425	LOCUS	AF133425	1044 bp	mrna	linear	PRI 16-NOV-1999
DEFINITION	Homo sapiens	tetraspanin TM4-C	mrna, complete cds.				
ACCESSION	AF133425						
VERSION	AF133425.1	GI:6434903					
KEYWORDS							
SOURCE	Homo sapiens (human)						

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 1044)
AUTHORS Pule,K.L., Ni,J., Liu,D., Morahan,G. and Wright,M.D.
TITLE The molecular characterization of four tetraspanins
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1044)
AUTHORS Pule,K.L., Ni,J., Liu,D. and Wright,M.D.
TITLE Direct Submission
JOURNAL Submitted (08-MAR-1999) Immunology, The Walter & Eliza Hall
Institute, Royal Parade, Parkville, Victoria 3031, Australia
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DB 221 CAATCGATGGGGCATCTTTCTGAAGATCTTCGGGGCACTGTCGCCAGTGCCATGCAGT 280
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QY 122 TGGGCTGTATGGTCTAAGACTGAGACAGTGTGGTCTTGGTCTTGGTCTTGGTCTTCC 181
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QY 182 TCCTCTCATCTTCAATGCTAGAGTGTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTCC 241
DB 401 TCCTCTCATCTTCAATGCTAGAGTGTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTCC 460
QY 242 TGGCTGAGCACTTCTCGAGTGTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTCC 287
DB 461 TGGCTGAGCACTTCTCGAGTGTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTCC 506
RESULT 8
CQ896240 1076 bp DNA linear PAT 05-NOV-2004
LOCUS Sequence 64 from Patent WO2004076614.
DEFINITION CQ896240
ACCESSION CQ896240
VERSION CQ896240.1 GI:55468089
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Hinzmann,B., Dahl,E., Rosenthal,A., Specht,T., Schmitt,A.,
Beckmann,G., Bruemendorf,T., Kinnemann,H., Roepcke,S., Hermann,K.,
Xinzhong,L., Pilarsky,C. and Staub,E.
TITLE Human nucleic acid sequences obtained from prostatic carcinomas

JOURNAL Patent: WO 2004076614-A 64 10-SEP-2004;
Hinzmann, Bernd (DE); Dahl, Edgar (DE); Rosenthal, Andre (DE);
Specht, Thomas (DE); Schmitt, Armin (DE)
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DB 158 TTGCTCAAGTGGGCTACTTCTCATCGACGCGCGTGTGGTCTTTGGCTCTTGGTTTCC 217
QY 122 TGGGCTGTCTATGGTCTAAGACTGAGACAGTGTGGTCTTGGTCTTGGTCTTGGTCTTCC 181
DB 218 TGGGCTGTCTATGGTCTAAGACTGAGACAGTGTGGTCTTGGTCTTGGTCTTGGTCTTCC 277
QY 182 TCCTCTCATCTTCAATGCTAGAGTGTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTCC 241
DB 278 TCCTCTCATCTTCAATGCTAGAGTGTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTCC 337
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DB 338 TGGCTGAGCACTTCTCGAGTGTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTGGTCTTCC 383
RESULT 9
AF054838 1076 bp mRNA linear PRI 03-NOV-1998
LOCUS Homo sapiens tetraspan TM4SP (TSPAN-1) mRNA, complete cds.
DEFINITION AF054838
ACCESSION AF054838.1 GI:2997740
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 1076)
AUTHORS Todd,S.C., Doctor,V.S. and Levy,S.
TITLE Sequences and expression of six new members of the
tetraspanin/TM4SP family
JOURNAL Blochim. Biophys. Acta 1399 (1), 101-104 (1998)
PUBMED 9714763
REFERENCE 2 (bases 1 to 1076)
AUTHORS Todd,S.C., Doctor,V.S. and Levy,S.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1998) Medicine, Stanford, 300 Pasteur, Stanford,
CA 94305-5115, USA
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Db	158	TTGTCAACGHTGGGCTACTTCTCATCGACGCCGGCGTGTGGTCTTGTCTTTGGTTTCC	217
Qy	122	TGGGCTGCTATGTGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGAAGTTCCTCTTCATCC	181
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RESULT 12
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DEFINITION Polynucleotides and polypeptides encoding receptors.
ACCESSION BD069061
VERSION BD069061.1 GI:22614664
KEYWORDS JP 2001509679-A/4.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE
1. (bases 1 to 1288)
AUTHORS Ni, J., Gentz, R.L. and Rosen, C.A.
TITLE Polynucleotides and polypeptides encoding receptors
JOURNAL HUMAN GENOME SCIENCES INC
COMMENT OS Unidentified
PN JP 2001509679-A/4
PD 24-JUL-2001
PF 21-JAN-1998 JP 1998534602
PR 21-JAN-1997 US 60/034204, 21-JAN-1997 US 60/034205 PI
JIAN NI, REINER L GENTZ, CRAIG A ROSEN
PC C12N15/12, C12N15/85, C12N5/10, C07K14/705, C07K16/28, C12Q1/68, PC A61K38/17.
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DB 215 CAATCGATGGGGCATCTTCTGAGATCTTCGGGCCACTGTCGCCAGTGCCATGCAGT 274
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QY 182 TCCTCTCATCTTCAATGCTGAGGTTCAGCTGCTGCTGCTGCCCTTGTGTACACCATAA 241
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DEFINITION Polynucleotides and polypeptides encoding receptors.
ACCESSION BD069078
VERSION BD069078.1 GI:22614681
KEYWORDS JP 2001509679-A/21.
SOURCE unidentified
ORGANISM unclassified.

unclassified.
1. (bases 1 to 1288)
AUTHORS Ni, J., Gentz, R.L. and Rosen, C.A.
TITLE Polynucleotides and polypeptides encoding receptors
JOURNAL HUMAN GENOME SCIENCES INC
COMMENT OS Unidentified
PN JP 2001509679-A/21
PD 24-JUL-2001
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PR 21-JAN-1997 US 60/034204, 21-JAN-1997 US 60/034205 PI
JIAN NI, REINER L GENTZ, CRAIG A ROSEN
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PC A61K48/00
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DB 954 TGGGCTGCTATGGTCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 895
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DB 894 TCCTCTCATCTTCAATGCTGAGGTTCAGCTGCTGCTGCTGCCCTTGTGTACACCATAA 835
QY 242 TGGCTGAGCACTTCCCGAGTGTGCTGGTAGTGCTGCCATCAAGAA 287
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RESULT 14
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LOCUS BD070259 1289 bp DNA linear PAT 27-AUG-2002
DEFINITION Compounds for immunodiagnosis of prostate cancer and methods for their use.
ACCESSION BD070259
VERSION BD070259.1 GI:22615862
KEYWORDS JP 2001513886-A/110.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 1289)
XU, J. and DILLON, D.C.
Compounds for immunodiagnosis of prostate cancer and methods for their use
Patent: JP 2001513886-A 110 04-SEP-2001;
CORIXA CORP
OS Homo sapiens (human)

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4322886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model
-Q=/abs/ABSSWEB_spool/US10079954/runat_23032006_102929_1793/app_query.fasta_1
-DB=UniProt -QMT=fastcan -SUFFIX=rup -MINWATCH=0.1 -LOOPCLR=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes02p
-USER=US10079954 -CGEN 1 1 580 @runat_23032006_102929_1793 -NCPU=6 -ICPU=3
-NO_MMAP -NRG_SCORES=0 -WAIT -DSFBLCK=100 -LONGLOG -DVG TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	453	80.3	241	1 TSNI1_HUMAN	Q50635 homo sapien
2	453	80.3	241	2 QSVST0_HUMAN	Q5vst0 homo sapien
3	450	79.8	241	1 TSNI1_PONPY	Q3rc27 pongo pygma
4	442	78.4	240	2 Q47M6_MACFA	Q4r7w6 macaca fasc
5	371	65.8	240	2 Q99J59_MOUSE	Q99j59 mus musculus
6	366	64.9	241	2 Q6AYR9_RAT	Q6ayr9 rattus norv
7	273.5	48.5	244	2 Q5HZ83_XENLA	Q5hz83 xenopus lae
8	270.5	48.0	244	2 Q6DDY1_XENLA	Q6ddy1 xenopus lae
9	221	39.2	240	2 Q6P420_XENLA	Q6p420 xenopus lae
10	210.5	37.3	234	2 Q7T2B8_BRARE	Q7t2b8 brachydanio
11	161	28.5	246	2 Q4RSJ3_TETNG	Q4rsj3 tetraodon n
12	158	28.0	225	2 Q569S1_XENLA	Q569s1 xenopus lae
13	158	28.0	247	2 Q9PT80_CHICK	Q9pte0 gallus gall
14	157.5	27.9	246	2 Q6DH58_BRARE	Q6dh58 brachydanio
15	157	27.8	247	2 Q6GP44_XENLA	Q6gp44 xenopus lae
16	157	27.8	265	2 Q802B9_XENLA	Q802b9 xenopus lae

17	155	27.5	249	1 TSNI1_BOVIN	Q58cy8 bos taurus
18	154.5	27.4	235	2 Q4S1G3_TETNG	Q4s1g3 tetraodon n
19	153	27.1	248	1 TSNI1_HUMAN	Q96a18 homo sapien
20	153	27.1	267	2 Q8WU1_HUMAN	Q8wu1 homo sapien
21	152.5	27.0	241	2 Q6DSC4_BRARE	Q6dsc4 brachydanio
22	151.5	26.9	231	2 Q5XGS2_XENLA	Q5xgs2 xenopus lae
23	149.5	26.5	238	1 TSNI1_HUMAN	Q14817 homo sapien
24	149.5	26.5	238	2 Q6IAP6_HUMAN	Q6iap6 homo sapien
25	149.5	26.5	238	2 Q5RAP3_PONPY	Q5rap3 pongo pygma
26	147.5	26.2	238	1 TSNI1_MOUSE	Q5dck3 mus musculus
27	147.5	26.2	238	2 Q5BR80_RAT	Q5br80 rattus norv
28	147.5	26.2	238	2 Q4FWU7_MOUSE	Q4fwu7 mus musculus
29	146.5	26.0	218	1 CD53_RAT	P24485 rattus norv
30	145.5	25.8	218	1 CD53_MOUSE	Q61451 mus musculus
31	145.5	25.8	248	1 TSNI1_MOUSE	Q80w1 mus musculus
32	144	25.5	217	2 Q6DCU4_XENLA	Q6dcu4 xenopus lae
33	143	25.4	236	2 Q9DSU7_BRARE	Q9dsu7 brachydanio
34	143	25.4	236	2 Q6PFU1_BRARE	Q6pfu1 brachydanio
35	141	25.0	211	2 Q9GLG9_SAGOE	Q9glg9 saguinus oe
36	141	25.0	236	1 CD81_CERAE	Q97703 cercopithec
37	141	25.0	236	1 CD81_HUMAN	P60033 homo sapien
38	141	25.0	236	1 CD81_MOUSE	P35762 mus musculus
39	141	25.0	236	1 CD81_PANTR	P60034 pan troglod
40	141	25.0	236	1 CD81_RAT	Q62745 rattus norv
41	141	25.0	236	1 CD81_SAGOE	Q9n039 saguinus oe
42	141	25.0	236	2 Q5U0J6_HUMAN	Q5u0j6 homo sapien
43	141	25.0	236	2 Q7YR89_9EUTH	Q7yr89 tupia chin
44	141	25.0	236	2 Q91V78_MOUSE	Q91v78 mus musculus
45	141	25.0	236	2 Q6P9V1_RAT	Q6p9v1 rattus norv

ALIGNMENTS

RESULT 1

TSNI1_HUMAN
ID TSNI1_HUMAN STANDARD; PRT; 241 AA.
AC O60635; O60745;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tetraspanin-1 (Tsphan-1) (Tetraspanin NET-1) (Tetraspanin TM4-C).
GN Names=TSN1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=98390278; PubMed=9714763; DOI=10.1016/S0167-4781(98)00087-6;
RA Todd S.C., Doctor V.S., Levy S.;
RT "Sequences and expression of six new members of the tetraspanin/TWASF family";
RL Blochim. Biophys. Acta 1399:101-104(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Rubinstein E., Serru V., Boucheix C.;
RT "New tetraspans identified in the EST database";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Puls K.L., Ni J., Liu D., Morahan G., Wright M.D.;
RT "The molecular characterization of four tetraspanins";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
Altschul S.F., Zeeberg F.S., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Pongo.
 OC NCB1_TaxID=9600;
 RN (1)
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Kidney;
 RG The German cDNA consortium;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
 CC
 CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 DR EMBL; CR858455; CAH90683.1; -; mRNA.
 DR InterPro; IPR000301; Tetraspanin 4.
 DR Pfam; PF00335; Tetraspanin; 1.
 DR PRINTS; PR00259; TMFOUR.
 DR PROSITE; PS00421; TM4_1; 1.
 KW Glycoprotein; Transmembrane.
 FT TOPO_DOM 1 11
 FT TRANSMEM 12 34
 FT TOPO_DOM 35 53
 FT TRANSMEM 54 76
 FT TOPO_DOM 77 88
 FT TRANSMEM 89 111
 FT TOPO_DOM 112 214
 FT TRANSMEM 215 237
 FT TOPO_DOM 238 241
 FT CARBOHYD 141 141
 FT CARBOHYD 154 154
 FT CARBOHYD 178 178
 FT CARBOHYD 184 184
 SQ SEQUENCE 241 AA; 26341 MW; BE029CDAD83F1139 CRC64;
 Alignment Scores:
 Pred. No.: 3,116-38 Length: 241
 Score: 450.00 Matches: 92
 Percent Similarity: 97.9% Conservative: 2
 Best Local Similarity: 95.8% Mismatches: 2
 Query Match: 79.8% Indels: 0
 DB: 1 Gaps: 0
 US-10-079-954-1 (1-297) x TSN1_PONPY (1-241)
 QY 1 GCAATCGATGGGCACTCTTCTGAAGATCTTCGGGCACTGTGTCAGTGCATGCAG 60
 Db 33 SerLeaspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerSerAlaMetGln 52
 QY 61 TTGTGCAACGTGGGCTACTTCTCATCGACGCGCGTGTGGTCTTCTTGGTTTC 120
 Db 53 PheValAsnValGlyTyrPheLeuLysAlaGlyValValPheAlaLeuGlyPhe 72
 QY 121 CTGGCTGCTATGCTGCTAAGACTGAGAGTGCCTGCTGCTGCTGCTGCTGCTGCT 180
 Db 73 LeuGlyCysTyrGlyAlaGlnThrGluSerLysCysAlaLeuMetThrPhePhePhe 92
 QY 181 CTCTCTCTCATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Db 93 LeuLeuLeuLeuPheLeuAlaGluValAlaAlaValValAlaLeuValTyrThr 112
 QY 241 ATGGCTGAGCACTTCCCGACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 288
 Db 113 MetAlaGluHiePheLeuThrLeuLeuValValProAlaLeuLysLys 128
 RESULT 4
 Q4R7W6_MACFA PRELIMINARY; PRT; 240 AA.

Q4R7W6;
 13-SEP-2005 (TrEMBLrel. 31, Created)
 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Testis cDNA clone: QtsA-14223, similar to human tetraspan 1 (TSPAN-1).
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 OX NCB1_TaxID=9541;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RA International consortium for macaque cDNA sequencing, analysis;
 RT "DNA sequences of macaque genes expressed in brain or testis and its evolutionary implications";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP NUCLEOTIDE SEQUENCE.
 RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y., Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
 RT "Substitution rate and structural divergence of 5'UTR evolution: Comparative analysis between human and cynomolgus monkey cDNAs";
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB168695; BAB0806.1; -; mRNA.
 SQ SEQUENCE 240 AA; 26243 MW; 5AB106570E958D3F CRC64;
 Alignment Scores:
 Pred. No.: 2,146-37 Length: 240
 Score: 442.00 Matches: 90
 Percent Similarity: 96.9% Conservative: 3
 Best Local Similarity: 93.8% Mismatches: 3
 Query Match: 78.4% Indels: 0
 DB: 2 Gaps: 0
 US-10-079-954-1 (1-297) x Q4R7W6_MACFA (1-240)
 QY 1 GCAATCGATGGGCACTCTTCTGAAGATCTTCGGGCACTGTGTCAGTGCATGCAG 60
 Db 33 SerLeaspGlyAlaSerPheLeuLysIlePheGlyProLeuSerSerSerAlaMetGln 52
 QY 61 TTGTGCAACGTGGGCTACTTCTCATCGACGCGCGTGTGGTCTTCTTGGTTTC 120
 Db 53 PheValAsnValGlyTyrPheLeuLysAlaGlyValValPheAlaLeuGlyPhe 72
 QY 121 CTGGCTGCTATGCTGCTAAGACTGAGAGTGCCTGCTGCTGCTGCTGCTGCTGCT 180
 Db 73 LeuGlyCysTyrGlyAlaGlnThrGluSerLysCysAlaLeuMetThrPhePhePhe 92
 QY 181 CTCTCTCTCATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Db 93 LeuLeuLeuLeuPheLeuAlaGluValAlaAlaValValAlaLeuValTyrThr 112
 QY 241 ATGGCTGAGCACTTCCCGACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 288
 Db 113 MetAlaGluHiePheLeuThrLeuLeuValValProAlaLeuLysLys 128
 RESULT 5
 Q99J59_MOUSE PRELIMINARY; PRT; 240 AA.
 ID Q99J59_MOUSE
 AC Q99J59;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Tetraspan 1 (Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030418M05 product:similar to tetraspan TSPAN-1).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCB1_TaxID=10090;

RN NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Klausner B.D., Collins R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk R.A.,
 RA Villalon D.K., Muzny N.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
 RA Director MGC Project;
 RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Asnburner M., Batalov S., Cabavant T.,
 RA Frieschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=22354693; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Oseto N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawai H., Kawaawa Y., Kedziercki R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wanstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=20530513; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN NP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=20530513; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami T., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yamanaka I., Yasunishi A.,
 RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
 RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC003448; AA03448.1; -; mRNA.
 DR EMBL; AK078869; BAC37431.1; -; mRNA.
 DR Ensembl; ENSMUSG0000028699; Mus musculus.
 DR MGI; MGI:1914055; Tapani.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016012; C:integral to membrane; TAS.
 DR InterPro; IPR002229; RhesusRHD.
 DR InterPro; IPR000301; Transmem. 4.
 DR Pfam; PF00335; Tetraspannin; 1.
 DR PRINTS; PR00342; RhesusRHD.
 DR PRINTS; PR00259; TMFOUR.
 DR PROSITE; PS00421; TM4.1; 1.
 SQ SEQUENCE 240 AA; 26356 MW; AD4C48A32BC2999 CRC64;

Alignment Scores:

GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
InterPro; IPR002229; RhesusRHD.
InterPro; IPR000301; Transmem 4.
Pfam; PF00335; Tetraspannin; I.
PRINTS; PR00342; RHESURHD.
PRINTS; PR00255; TMPOUR.
PROSITE; PS00421; TM4_1; 1.
SEQUENCE 241 AA; 26453 MW; 911B8E65464D1A70 CRC64;

Alignment Scores:
Pred. No.: 2e-29 Length: 241
Score: 366.00 Matches: 73
Percent Similarity: 85.4% Conservative: 9
Best Local Similarity: 76.0% Mismatches: 14
Query Match: 64.9% Indels: 0
DB: 2 Gaps: 0

US-10-079-954-1 (1-297) x Q6AYR9_RAT (1-241)

QY 1 GCAATCGATGGGCACTCTTTTCTGAAGATCTTCGGGCCACTGTGTCGATGCCATGCAG 60
Db : : : : :
Db 33 SerValaspGlyThrSerPheLeuLysAlaPheGlySerLeuSerSerAlaMetGln 52

QY 61 TTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGCTTGTTGGTCTTTGCTCTTGGTTTC 120
Db PheValAsnValGlyTyrrPheLeuIleAlaAlaGlyAlaValLeuPheIleLeuGlyPhe 72

QY 121 CTGGCGTCTATCGTCTTAAGACTGTGAGCAAGTGCCTCGNGACGTTCTTCTTCATC 180
Db : : : : :
Db 73 LeuGlyCystrGlyAlaHisrGluAsnLysCysValLeuMetMetPhePheSerIle 92

QY 181 CTCCTCTCATCTTCATTGCTGAGGTTGTCAGCTGCTGTGGTGCCTTGGTGTACACCATA 240
Db : : : : :
Db 93 LeuLeuIlellePheIleAlaGluIleAlaGlyAlaValValAlaLeuValTyrrThr 112

QY 241 ATGGCTGAGCACTTCCGACGTTGCTGGTAGTGCTGCCATCAAGAAG 288
Db : : : : :
Db 113 MetAlaGluGlnPheLeuThrrPheLeuValValProAlaIleGluLys 128

RESULT 7
QSHZS3 XENLA PRELIMINARY; PRT; 244 AA.

ID QSHZS3 XENLA AC
QSHZS3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE LOC496318 protein.
GN Names=LOC496318;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Egg;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strauberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RA RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Egg;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Ziesberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

```
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Egg;
RC Klein S., Gerhard D.S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC088907; AA88907.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR000301; Transmem_4.
DR Pfam; PF00335; Tetraspannin; I.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4.1; 1.
SQ SEQUENCE 244 AA; 26350 MW; D83087612DF052CE CRC64;

Alignment Scores:
Pred. No.: 1e-19 Length: 244
Score: 273.50 Matches: 58
Percent Similarity: 76.8% Conservative: 18
Best Local Similarity: 58.6% Mismatches: 18
Query Match: 48.5% Indels: 5
DB: 2 Gaps: 2

US-10-079-954-1 (1-297) x Q5HSZ3_XENLA (1-244)
QY 1 GCATCGATGGGCATCTCTTCTGAGATCTTCGGGCCACTGTGG---TCCAGTGCCTATG 57
DB 33 SerValAspSerAsnSerPheLeuIleAlaGlyThrValSerAlaSerAlaVal 52
QY 58 CAGTTTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTGTGGTCTTGTCTTGGT 117
DB 53 GlnPheValAsnValGlyTyrPheLeuIleAlaGlyAlaLeuValLeuGly 72
QY 118 TTCCTGGGCTGCTATGCTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGCCTTCTTC 177
DB 73 PheLeuGlyCysCysGlyAlaGlnLysGluSerLysCysLeuLeuIlePhePheThr 92
QY 178 ATCTCTCTCTCATCTTCTCATGCTGAGTTGCGAGTGTGCTGCTGCTGCTGCTAC 237
DB 93 IleIleLeuIlePheIleAlaGluValAlaGlyAlaValAlaLeuValTyrSer 112
QY 238 ATAATGGCTGAGCACTTCCCGACGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 294
DB 113 AsnLeuAlaGluSer-----IleLeuGlyProLeuLeuIleProValLeu 127

RESULT 8
Q6DDY1_XENLA
ID Q6DDY1_XENLA PRELIMINARY; PRT; 244 AA.
AC Q6DDY1
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MGC81526 protein.
GN Name=MGC81526;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus;
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
```

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RC TISSUE=Embryo;
RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RC Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC077370; AA877370.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR002229; RhesusRHD.
DR Pfam; PF00335; Tetraspannin; 1.
DR PRINTS; PR00342; RHEUSRHD.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4.1; 1.
SQ SEQUENCE 244 AA; 26408 MW; FC2D8CC250644E99 CRC64;

Alignment Scores:
Pred. No.: 2.07e-19 Length: 244
Score: 270.50 Matches: 57
Percent Similarity: 76.8% Conservative: 19
Best Local Similarity: 57.6% Mismatches: 18
Query Match: 48.0% Indels: 5
DB: 2 Gaps: 2

US-10-079-954-1 (1-297) x Q6DDY1_XENLA (1-244)
QY 1 GCATCGATGGGCATCTCTTCTGAGATCTTCGGGCCACTGTGG---TCCAGTGCCTATG 57
DB 33 SerValAspSerAsnSerPheLeuIleAlaGlyThrValSerAlaSerAlaVal 52
QY 58 CAGTTTGTCAACGTGGGCTACTTCTCATCGCAGCGCGGTGTGGTCTTGTCTTGGT 117
DB 53 GlnPheValAsnValGlyTyrPheLeuIleAlaGlyAlaLeuValLeuGly 72
QY 118 TTCCTGGGCTGCTATGCTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGCCTTCTTC 177
DB 73 PheLeuGlyCysCysGlyAlaGlnLysGluSerLysCysLeuLeuIlePhePheThr 92
QY 178 ATCTCTCTCTCATCTTCTCATGCTGAGTTGCGAGTGTGCTGCTGCTGCTGCTAC 237
DB 93 IleIleLeuIlePheIleAlaGluValAlaGlyAlaValAlaLeuValTyrSer 112
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Qy 238 ATAATGGCTGACCACTTCCCGACGTTGCTGTAGTGGCTCCATCAGAGATATG 239
 Db 113 SerLeuAlaGlusr-----fLeuGlyProLeuLeuysProValLeu 120
 RESULT 9
 Q6P420_XENLA PRELIMINARY; PRT; 240 AA.
 ID O6P420_XENLA PRELIMINARY; PRT; 240 AA.
 AC Q6P420;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE MGCG68536 protein.
 DE MGCG68536 protein.
 GN Name-MGC68536;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McGowan P.J.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J.J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RP [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RT Dev. Dyn. 225:384-391 (2002).
 RP [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RA Klein S., Strausberg R.;
 RA Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC063728; AAH63728.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR000301; Transmem_4.
 DR Pfam; PF00335; Tetraspanin; 1.
 DR PRINTS; PR00259; TMFOUR.
 DR PROSITE; PS00421; TW4 1; 1.
 SQ SEQUENCE 240 AA; 25979 MW; 1AA7CA4F3C76E376 CRC64;
 Alignment Scores:
 Pred. No.: 3.2e-14 Length: 240
 Score: 621.00 Matches: 43
 Percent Similarity: 69.0% Conservative: 15
 Best Local Similarity: 51.2% Mismatches: 26
 Query Match: 39.2% Indels: 0
 DB: 2 Gaps: 0

SQ SEQUENCE 234 AA; 24894 MW; E713846FE750C054 CRC64;

Alignment Scores:

Pred. No.: 4.03e-13 Length: 234
Score: 210.50 Matches: 48
Percent Similarity: 60.6% Conservative: 12
Best Local Similarity: 48.5% Mismatches: 36
Query Match: 37.3% Indels: 3
DB: 2 Gaps: 1

US-10-079-954-1 (1-297) x Q7T2B8_BRARE (1-234)

```
QY 4 ATCGATGGGCATCTCTTCTGAAGATCTTCGGGCCACTG-----TCGTCCAGTGCC 54
DB ValAspAenglyserileleuasnPhemetGlnSerLeuProGlyAlaserSerGlnMet 44
QY 55 ATCGAGTTTGTCAACGTGGGTACTTCTCATCGCAGCGCGGTGTGTGCTTCTTCTT 114
DB 45 GlyGlnValLeuasnValGlyTyrLeuLeuileAlaLeuGlyAlaValValLeu 64
QY 115 GGTTCCTGGGTGCTATGGTCTAAGACTGAGACAAAGTGGCCCTCGTACGTTCTTC 174
DB 65 GlyPheLeuGlyCysCysGlyAlaileLysGlnSerArgCysMetLeuMetLeuPhe 84
QY 175 TTCATCCTCCTCATCTTCTGAGTTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 234
DB 85 IleIleIleLeuileilePheileAlaGluValAlaGlyAlaileValleLeuAlaPhe 104
QY 235 ACCATAATGGCTGAGCACTTCCCGACGTTGTGTGTGTGTGTGTGTGTGTGTGTGT 291
DB 105 ArgProLeuAlaGluThrLeuileLysGlnLeuGlyValAspAlaValLysSerLeu 123
```

RESULT 11

```
QY QARS3 TETNG
AC QARS3 TETNG PRELIMINARY; PRT; 246 AA.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Chromosome 13 SCAP15000, whole genome shotgun sequence.
GN ORFNames=GSTENG00029794001;
OC Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Maucell E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicod S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Croallius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: the sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01015000; CAG08729.1; -; Genomic DNA.
SQ SEQUENCE 246 AA; 27564 MW; AD91A3397819D50A CRC64;
```

Alignment Scores:

Pred. No.: 6.29e-08 Length: 246
Score: 161.00 Matches: 34
Percent Similarity: 66.3% Conservative: 23
Best Local Similarity: 39.5% Mismatches: 23
Query Match: 28.5% Indels: 6
DB: 2 Gaps: 3

US-10-079-954-1 (1-297) x Q4RSA3_TETNG (1-246)

```
QY 4 ATCGATGGGCATCTCTTCTGAAGATCTTCGGGCCACTGTCGTCACATGCATGATTT 63
DB ValAspProThrGlyPheArgGluile-----IleAlaAlaAsnProLeuPhe 52
QY 64 GTCACGTGGGTACTTCTCATCGCAGCGCGGTGTGTGCTTCTTGTGTTCTGCTG 123
DB 53 ThrGlyVal---TyrValIleLeuGlyLeuGlyMetLeuPheLeuGlyPheLeu 71
QY 124 GGCTGCTATGCTGAAGACTGAGACAAAGTGGCCCTCGTACGTTCTTCTTCATCTC 183
DB 72 GlyCysGlyAlaileArgGluasnLysCysLeuLeuPhePheMetLeuile 91
QY 184 CTCCTCATCTTCTATGCTGAGTTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 237
DB 92 LeuLeuilePheLeuAlaGluLeuAlaAlaileLeuAlaPheilePheArgGluHis 111
QY 238 ATAATGGCTGACGACTTC 255
DB 112 LeuThrArgGluTyrPhe 117
```

RESULT 12

```
QY Q569S1_XENLA PRELIMINARY; PRT; 225 AA.
AC Q569S1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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DR Pfam: PF00335; Tetraspannin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00212; ALBUMIN; UNKNOWN 1.
SQ SEQUENCE 246 AA; 27882 MW; 0713309E00CE0B35 CRC64;

Alignment Scores:
Pred. No.: 1.47e-07 Length: 246
Score: 157.50 Matches: 35
Percent Similarity: 61.1% Conservative: 23
Best Local Similarity: 36.8% Mismatches: 30
Query Match: 27.9% Indels: 7
DB: 2 Gaps: 3

US-10-079-954-1 (1-297) x Q6DH58_BRARE (1-246)
QY 4 ATCGATGGGCATCTCTTCTGAAGATCTTCGGGCCACTGTGTCGACGTCGCATGTCAGTTT 63
DB 36 ValAspProThrGlyPheArgGluile-----ValAlaAlaAsnProLeuLeuPhe 52
QY 64 GTCAACGTGGGCTACTTCTCATCGACCGCGGCGTGTGCTTGTCTTCTGTTTCTCTG 123
DB 53 ThrGlyVal---TyrIleileLeuAlaMetGlyGlyMetLeuPheLeuGlyPheLeu 71
QY 124 GCCTGCTATGGTCTAAGACTGAGACGAGTGTGCCCTCGACGTTCTTCTTCATCCTC 183
DB 72 GlyCysCysArgAlaileArgGluAsnLysCysLeuLeuLeuPhePheMetLeuile 91
QY 184 CTCTCATCTTCATTTCTGAGTGTGTCGCGCTGTCGTCGTCGTCATCATATG 243
DB 92 LeuileilePheLeuAlaGluLeuAlaAlaileleLeuAlaPheilePhe----- 108
QY 244 GCTGACGACTTCCCGACGTTGCTGTGTAGTGCCTGCTGCATCAAGAG 288
DB 109 ArgGluHisLeuThrArgGluLufyrPheThrLysGluLeuLysLys 123

RESULT 15
QG6P44_XENLA PRELIMINARY; PRT; 247 AA.
AC Q6GP44;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LOC398586 protein.
GN Name=LOC398586;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore S., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Spleen;
RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RX Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S.L., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073301; AAH73301.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005764; C:lysosome; IEA.
DR InterPro; IPR00264; Serum albumin.
DR InterPro; IPR00301; Transmem 4.
DR Pfam; PF00335; Tetraspannin; I.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00212; ALBUMIN; UNKNOWN 1.
DR PROSITE; PS00421; TM4 1; 1.
SQ SEQUENCE 247 AA; 27657 MW; 05EB39416D66C085 CRC64;

Alignment Scores:
Pred. No.: 1.65e-07 Length: 247
Score: 157.00 Matches: 31
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Best Local Similarity: 40.3% Mismatches: 20
Query Match: 27.8% Indels: 4
DB: 2 Gaps: 2

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QY 64 GTCAACGTGGGCTACTTCTCATCGACCGCGGCGTGTGCTTGTGCTTGTGTTTCTCTG 123
DB 53 Ilegly--AlaTyrLeuValLeuAlaMetGlyGlyMetLeuPheLeuGlyPheLeu 71
QY 124 GCCTGCTATGGTCTAAGACTGAGACGAGTGTGCCCTCGACGTTCTTCTTCATCCTC 183
DB 72 GlyCysCysGlyAlaileArgGluAsnLysCysLeuLeuValPhePheMetPheile 91
QY 184 CTCTCATCTTCATTTCTGAGTGTGTCGCGCTGTCGTCGTCGTCATCATGTC 234
DB 92 LeuMetilePheLeuAlaGluLeuSerAlaAlaileLeuAlaPheLeuPhe 108

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Job time : 98.2097 secs
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